GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 12:14:52 ; Search time 332 Seconds
(without alignments)
72.922 Million cell updates/sec

Title: US-10-748-475-1
Perfect score: 4
Sequence: 1 uuyg 4

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_NA:*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3.6	90.0	4	9	US-09-886-223-9	Sequence 9, Appli
	2	3.6	90.0	4	13	US-10-027-632-52979	Sequence 52979, A
c	3	3.6	90.0	4	13	US-10-027-632-177980	Sequence 177980,
c	4	3.6	90.0	4	13	US-10-027-632-177997	Sequence 177997,
c	5	3.6	90.0	4	13	US-10-027-632-178014	Sequence 178014,
c	6	3.6	90.0	4	13	US-10-027-632-178297	Sequence 178297,
c	7	3.6	90.0	4	13	US-10-027-632-178309	Sequence 178309,
c	8	3.6	90.0	4	13	US-10-027-632-178364	Sequence 178364,
c	9	3.6	90.0	4	13	US-10-027-632-178378	Sequence 178378,
c	10	3.6	90.0	4	13	US-10-027-632-178393	Sequence 178393,
c	11	3.6	90.0	4	13	US-10-027-632-178423	Sequence 178423,
c	12	3.6	90.0	4	13	US-10-027-632-178425	Sequence 178425,
c	13	3.6	90.0	4	13	US-10-027-632-178511	Sequence 178511,
c	14	3.6	90.0	4	13	US-10-027-632-178519	Sequence 178519,
c	15	3.6	90.0	4	13	US-10-027-632-178527	Sequence 178527,
c	16	3.6	90.0	4	13	US-10-027-632-178577	Sequence 178577,
c	17	3.6	90.0	4	13	US-10-027-632-178588	Sequence 178588,
c	18	3.6	90.0	4	13	US-10-027-632-178602	Sequence 178602,
c	19	3.6	90.0	4	13	US-10-027-632-178672	Sequence 178672,
	20	3.6	90.0	4	17	US-10-027-632-52979	Sequence 52979, A
c	21	3.6	90.0	4	17	US-10-027-632-177980	Sequence 177980,
c	22	3.6	90.0	4	17	US-10-027-632-177997	Sequence 177997,
c	23	3.6	90.0	4	17	US-10-027-632-178014	Sequence 178014,
c	24	3.6	90.0	4	17	US-10-027-632-178297	Sequence 178297,
c	25	3.6	90.0	4	17	US-10-027-632-178309	Sequence 178309,
c	26	3.6	90.0	4	17	US-10-027-632-178364	Sequence 178364,
c	27	3.6	90.0	4	17	US-10-027-632-178378	Sequence 178378,
c	28	3.6	90.0	4	17	US-10-027-632-178393	Sequence 178393,
c	29	3.6	90.0	4	17	US-10-027-632-178423	Sequence 178423,
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c	32	3.6	90.0	4	17	US-10-027-632-178519	Sequence 178519,
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c	35	3.6	90.0	4	17	US-10-027-632-178588	Sequence 178588,
c	36	3.6	90.0	4	17	US-10-027-632-178602	Sequence 178602,
c	37	3.6	90.0	4	17	US-10-027-632-178672	Sequence 178672,
	38	3.6	90.0	4	17	US-10-618-963-9	Sequence 9, Appli
	39	3.6	90.0	4	18	US-10-748-475-1	Sequence 1, Appli
	40	3.6	90.0	4	18	US-10-748-475-7	Sequence 7, Appli
	41	3.6	90.0	4	18	US-10-836-670-57	Sequence 57, Appl
	42	3.6	90.0	5	14	US-10-172-620-4	Sequence 4, Appli
c	43	3.6	90.0	5	16	US-10-041-860-110	Sequence 110, App
c	44	3.6	90.0	5	17	US-10-407-846-5	Sequence 5, Appli
	45	3.6	90.0	5	18	US-10-673-938-23	Sequence 23, Appl
	46	3.6	90.0	5	18	US-10-673-938-29	Sequence 29, Appl
	47	3.6	90.0	6	8	US-08-887-505-106	Sequence 106, App
c	48	3.6	90.0	6	9	US-09-320-337-12	Sequence 12, Appl
	49	3.6	90.0	6	9	US-09-735-363A-23	Sequence 23, Appl
	50	3.6	90.0	6	9	US-09-735-363A-72	Sequence 72, Appl
	51	3.6	90.0	6	9	US-09-879-668-3	Sequence 3, Appli
	52	3.6	90.0	6	10	US-09-888-326-210	Sequence 210, App
	53	3.6	90.0	6	10	US-09-776-479-646	Sequence 646, App
	54	3.6	90.0	6	11	US-09-776-479-646	Sequence 646, App
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c	56	3.6	90.0	6	13	US-10-133-888-3	Sequence 3, Appli
c	57	3.6	90.0	6	13	US-10-133-888-8	Sequence 8, Appli
c	58	3.6	90.0	6	13	US-10-133-888-9	Sequence 9, Appli
c	59	3.6	90.0	6	13	US-10-133-888-10	Sequence 10, Appl
c	60	3.6	90.0	6	13	US-10-133-888-11	Sequence 11, Appl
c	61	3.6	90.0	6	13	US-10-133-888-17	Sequence 17, Appl
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c	63	3.6	90.0	6	13	US-10-133-888-19	Sequence 19, Appl
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c	65	3.6	90.0	6	13	US-10-027-632-52896	Sequence 52896, A
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	67	3.6	90.0	6	13	US-10-027-632-52936	Sequence 52936, A
c	68	3.6	90.0	6	13	US-10-027-632-53495	Sequence 53495, A
	69	3.6	90.0	6	13	US-10-027-632-58547	Sequence 58547, A
c	70	3.6	90.0	6	13	US-10-027-632-178012	Sequence 178012,
	71	3.6	90.0	6	14	US-10-092-908-18	Sequence 18, Appl
	72	3.6	90.0	6	14	US-10-112-653-620	Sequence 620, App
	73	3.6	90.0	6	14	US-10-017-995-646	Sequence 646, App
	74	3.6	90.0	6	14	US-10-229-208-16	Sequence 16, Appl
c	75	3.6	90.0	6	14	US-10-229-208-16	Sequence 16, Appl
c	76	3.6	90.0	6	15	US-10-235-113-38	Sequence 38, Appl
	77	3.6	90.0	6	15	US-10-253-117-21	Sequence 21, Appl
c	78	3.6	90.0	6	15	US-10-253-117-21	Sequence 21, Appl
	79	3.6	90.0	6	15	US-10-280-274-3	Sequence 3, Appli
	80	3.6	90.0	6	16	US-10-041-860-100	Sequence 100, App
	81	3.6	90.0	6	16	US-10-041-860-103	Sequence 103, App
	82	3.6	90.0	6	16	US-10-041-860-115	Sequence 115, App
	83	3.6	90.0	6	16	US-10-041-860-134	Sequence 134, App
	84	3.6	90.0	6	16	US-10-041-860-150	Sequence 150, App

85	3.6	90.0	6	16	US-10-041-860-182	Sequence 182, App
c 86	3.6	90.0	6	16	US-10-041-860-195	Sequence 195, App
c 87	3.6	90.0	6	16	US-10-190-312A-218	Sequence 218, App
c 88	3.6	90.0	6	16	US-10-190-312A-306	Sequence 306, App
89	3.6	90.0	6	16	US-10-190-312A-335	Sequence 335, App
c 90	3.6	90.0	6	16	US-10-190-312A-346	Sequence 346, App
c 91	3.6	90.0	6	17	US-10-027-632-52896	Sequence 52896, A
92	3.6	90.0	6	17	US-10-027-632-52928	Sequence 52928, A
93	3.6	90.0	6	17	US-10-027-632-52936	Sequence 52936, A
c 94	3.6	90.0	6	17	US-10-027-632-53495	Sequence 53495, A
95	3.6	90.0	6	17	US-10-027-632-58547	Sequence 58547, A
c 96	3.6	90.0	6	17	US-10-027-632-178012	Sequence 178012,
97	3.6	90.0	6	17	US-10-314-578-646	Sequence 646, App
c 98	3.6	90.0	6	17	US-10-317-444-513	Sequence 513, App
99	3.6	90.0	6	17	US-10-317-444-514	Sequence 514, App
100	3.6	90.0	6	17	US-10-332-914-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-886-223-9
; Sequence 9, Application US/09886223
; Patent No. US20020028458A1
; GENERAL INFORMATION:
; APPLICANT: LEXOW, Preben
; TITLE OF INVENTION: SEQUENCING METHOD USING MAGNIFYING TAGS
; FILE REFERENCE: Q-64884
; CURRENT APPLICATION NUMBER: US/09/886,223
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/GB99/04417
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: NO 19996339
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: NO 19996338
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: NO 19996337
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: NO 19996336
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: NO 19996335
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: NO 19996334
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: NO 19996333
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: NO 19996332
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: NO 19996331
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: NO 19996330
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: NO 19986133
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-886-223-9

Query Match 90.0%; Score 3.6; DB 9; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTG 4
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RESULT 2
US-10-027-632-52979
; Sequence 52979, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52979
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52979

Query Match 90.0%; Score 3.6; DB 13; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTCG 4
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RESULT 3
US-10-027-632-177980/c
; Sequence 177980, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177980
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-177980

Query Match 90.0%; Score 3.6; DB 13; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db          4 TTTG 1
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RESULT 4
US-10-027-632-177997/c
; Sequence 177997, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177997
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-177997

Query Match 90.0%; Score 3.6; DB 13; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db          4 TTTG 1
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RESULT 5
US-10-027-632-178014/c
; Sequence 178014, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178014
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178014

Query Match 90.0%; Score 3.6; DB 13; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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              :::|
Db          4 TTTG 1
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RESULT 6
US-10-027-632-178297/c
; Sequence 178297, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178297
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178297

Query Match 90.0%; Score 3.6; DB 13; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db          4 TTTG 1
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RESULT 7
US-10-027-632-178309/c
; Sequence 178309, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

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;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178309
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178309

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 8
US-10-027-632-178364/c
; Sequence 178364, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178364
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178364

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 9
US-10-027-632-178378/c
; Sequence 178378, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178378
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178378

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 10
US-10-027-632-178393/c
; Sequence 178393, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178393
;   LENGTH: 4
;   TYPE: DNA
```

```
;   ORGANISM: Human
US-10-027-632-178393

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 11
US-10-027-632-178423/c
; Sequence 178423, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178423
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178423

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 12
US-10-027-632-178425/c
; Sequence 178425, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178425
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178425

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 13
US-10-027-632-178511/c
; Sequence 178511, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178511
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178511

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 14
US-10-027-632-178519/c
; Sequence 178519, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
```

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;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178519
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178519

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 15
US-10-027-632-178527/c
; Sequence 178527, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178527
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178527

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 16
US-10-027-632-178577/c
; Sequence 178577, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178577
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178577

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 17
US-10-027-632-178588/c
; Sequence 178588, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178588
```

```
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178588

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 18
US-10-027-632-178602/c
; Sequence 178602, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178602
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178602

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 19
US-10-027-632-178672/c
; Sequence 178672, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178672
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178672

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 20
US-10-027-632-52979
; Sequence 52979, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52979
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-52979

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 21
US-10-027-632-177980/c
; Sequence 177980, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
```

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;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177980
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-177980

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 22
US-10-027-632-177997/c
; Sequence 177997, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 177997
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-177997

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 23
US-10-027-632-178014/c
; Sequence 178014, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178014
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178014

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 24
US-10-027-632-178297/c
; Sequence 178297, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178297
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178297

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 25
US-10-027-632-178309/c
; Sequence 178309, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178309
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178309

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 26
US-10-027-632-178364/c
; Sequence 178364, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178364
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178364

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 27
US-10-027-632-178378/c
; Sequence 178378, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178378
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-178378

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 28
US-10-027-632-178393/c
; Sequence 178393, Application US/10027632
; Publication No. US20030204075A9
```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178393
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178393

Query Match 90.0%; Score 3.6; DB 17; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 29
US-10-027-632-178423/c
; Sequence 178423, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178423
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178423

Query Match 90.0%; Score 3.6; DB 17; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 30
US-10-027-632-178425/c
; Sequence 178425, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178425
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178425

Query Match 90.0%; Score 3.6; DB 17; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 31
US-10-027-632-178511/c
; Sequence 178511, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

```
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178511
;    LENGTH: 4
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-178511

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 32
US-10-027-632-178519/c
; Sequence 178519, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178519
;    LENGTH: 4
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-178519

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 33
US-10-027-632-178527/c
; Sequence 178527, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178527
;    LENGTH: 4
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-178527

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 34
US-10-027-632-178577/c
; Sequence 178577, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178577
;    LENGTH: 4
;    TYPE: DNA
;    ORGANISM: Human
US-10-027-632-178577

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 35
US-10-027-632-178588/c
```

; Sequence 178588, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178588
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178588

Query Match 90.0%; Score 3.6; DB 17; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 36
US-10-027-632-178602/c
; Sequence 178602, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178602
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178602

Query Match 90.0%; Score 3.6; DB 17; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 37
US-10-027-632-178672/c
; Sequence 178672, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178672
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178672

Query Match 90.0%; Score 3.6; DB 17; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.4e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 38
US-10-618-963-9
; Sequence 9, Application US/10618963
; Publication No. US20040076998A1
; GENERAL INFORMATION:
; APPLICANT: LEXOW, Preben
; TITLE OF INVENTION: SEQUENCING METHOD USING MAGNIFYING TAGS
; FILE REFERENCE: Q-64884
; CURRENT APPLICATION NUMBER: US/10/618,963
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/886,223
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/GB99/04417
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: NO 19996339
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: NO 19996338
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: NO 19996337
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: NO 19996336
; PRIOR FILING DATE: 1999-06-11

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;  PRIOR APPLICATION NUMBER: NO 19996335
;  PRIOR FILING DATE: 1999-04-19
;  PRIOR APPLICATION NUMBER: NO 19996334
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: NO 19996333
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: NO 19996332
;  PRIOR FILING DATE: 1999-04-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: synthetic construct
US-10-618-963-9

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 1.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 39
US-10-748-475-1
; Sequence 1, Application US/10748475
; Publication No. US20040138166A1
; GENERAL INFORMATION:
;  APPLICANT: Damha, Masad  J.
;  APPLICANT:  Hannoush, Rami  N.
;  APPLICANT:  Min, Kyung-Lyum
;  APPLICANT:  Carriero, Sandra
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING RNASE H ACTIVITY OF RETRO
;  TITLE OF INVENTION:  REVERSE TRANSCRIPTASE
;  FILE REFERENCE: MGU-0025
;  CURRENT APPLICATION NUMBER: US/10/748,475
;  CURRENT FILING DATE:  2003-12-30
;  PRIOR APPLICATION NUMBER: US 60/437,568
;  PRIOR FILING DATE: 2002-12-31
;  PRIOR APPLICATION NUMBER: US 60/509,716
;  PRIOR FILING DATE: 2003-10-07
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic loop moiety
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: "Y" represents "C" or "U"
US-10-748-475-1

  Query Match             90.0%;  Score 3.6;  DB 18;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+09;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              ||||
Db          1 UUYG 4


RESULT 40
US-10-748-475-7
; Sequence 7, Application US/10748475
; Publication No. US20040138166A1
; GENERAL INFORMATION:
;  APPLICANT: Damha, Masad  J.
;  APPLICANT:  Hannoush, Rami  N.
;  APPLICANT:  Min, Kyung-Lyum
;  APPLICANT:  Carriero, Sandra
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING RNASE H ACTIVITY OF RETRO
;  TITLE OF INVENTION:  REVERSE TRANSCRIPTASE
;  FILE REFERENCE: MGU-0025
;  CURRENT APPLICATION NUMBER: US/10/748,475
;  CURRENT FILING DATE:  2003-12-30
;  PRIOR APPLICATION NUMBER: US 60/437,568
;  PRIOR FILING DATE: 2002-12-31
;  PRIOR APPLICATION NUMBER: US 60/509,716
;  PRIOR FILING DATE: 2003-10-07
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 4
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic loop moiety
US-10-748-475-7

  Query Match             90.0%;  Score 3.6;  DB 18;  Length 4;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+09;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              ||:|
Db          1 UUCG 4


RESULT 41
US-10-836-670-57
; Sequence 57, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
;  APPLICANT: Schultz, Gregory Scott
;  APPLICANT:  Lewin, Alfred Samuel
;  APPLICANT:  Blalock, Timothy D.
;  TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
;  FILE REFERENCE: 5853-303
;  CURRENT APPLICATION NUMBER: US/10/836,670
;  CURRENT FILING DATE:  2004-04-30
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 4
;   TYPE: RNA
;   ORGANISM: Human adenovirus type 1
US-10-836-670-57

  Query Match             90.0%;  Score 3.6;  DB 18;  Length 4;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+09;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              ||:|
Db          1 UUCG 4


RESULT 42
US-10-172-620-4
; Sequence 4, Application US/10172620
; Publication No. US20030053995A1
; GENERAL INFORMATION:
;  APPLICANT: Hung, Mien-Chie
;  APPLICANT:  Lin, Shiaw-Yih
;  TITLE OF INVENTION: Methods and Compositions for Inhibiting EGF Receptor
;  FILE REFERENCE: UTSC:720US
;  CURRENT APPLICATION NUMBER: US/10/172,620
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/298,579
;  PRIOR FILING DATE: 2001-06-15
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;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Human
US-10-172-620-4

  Query Match             90.0%;  Score 3.6;  DB 14;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 1.1e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 43
US-10-041-860-110/c
; Sequence 110, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-041-860-110

  Query Match             90.0%;  Score 3.6;  DB 16;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 1.1e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 1


RESULT 44
US-10-407-846-5/c
; Sequence 5, Application US/10407846
; Publication No. US20040038258A1
; GENERAL INFORMATION:
;  APPLICANT: HARLEY, JOHN B.
;  APPLICANT:  KAUFMAN, KENNETH M.
;  TITLE OF INVENTION: METHODS FOR DETECTING DNA POLYMORPHISMS
;  FILE REFERENCE: OMRF:010US
;  CURRENT APPLICATION NUMBER: US/10/407,846
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: 60/376,360
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-10-407-846-5

  Query Match             90.0%;  Score 3.6;  DB 17;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 1.1e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 45
US-10-673-938-23
; Sequence 23, Application US/10673938
; Publication No. US20040152108A1
; GENERAL INFORMATION:
;  APPLICANT: Keith, Jonathan M
;  APPLICANT:  Bryant, Darryn E
;  APPLICANT:  Adams, Peter
;  TITLE OF INVENTION: A method for sequence analysis
;  FILE REFERENCE: 2512891
;  CURRENT APPLICATION NUMBER: US/10/673,938
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: PCT/AU02/00397
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: USSN 60/279,238
;  PRIOR FILING DATE: 2001-03-28
;  NUMBER OF SEQ ID NOS: 188
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 5
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Sequence string
US-10-673-938-23

  Query Match             90.0%;  Score 3.6;  DB 18;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 1.1e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTCG 5


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Job time : 336 secs
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:53:27 ; Search time 95 Seconds
(without alignments)
68.896 Million cell updates/sec

Title: US-10-748-475-1
Perfect score: 4
Sequence: 1 uuyg 4

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	3.6	90.0	4	4	US-09-886-223-9	Sequence 9, Appli
c	3	3.6	90.0	5	2	US-08-587-332B-11	Sequence 11, Appl
c	4	3.6	90.0	5	3	US-08-855-372B-9	Sequence 9, Appli
c	5	3.6	90.0	5	3	US-09-498-851-9	Sequence 9, Appli
	6	3.6	90.0	6	1	US-08-683-045-10	Sequence 10, Appl
	7	3.6	90.0	6	1	US-08-393-888-17	Sequence 17, Appl
	8	3.6	90.0	6	1	US-08-463-288A-48	Sequence 48, Appl
	9	3.6	90.0	6	2	US-08-470-445A-48	Sequence 48, Appl
	10	3.6	90.0	6	2	US-08-462-679-48	Sequence 48, Appl
	11	3.6	90.0	6	2	US-08-466-210A-48	Sequence 48, Appl
	12	3.6	90.0	6	2	US-08-485-158A-2	Sequence 2, Appli
	13	3.6	90.0	6	2	US-08-467-147A-48	Sequence 48, Appl
	14	3.6	90.0	6	2	US-08-469-014-48	Sequence 48, Appl
c	15	3.6	90.0	6	2	US-08-442-809A-12	Sequence 12, Appl
c	16	3.6	90.0	6	3	US-08-973-568-50	Sequence 50, Appl
c	17	3.6	90.0	6	3	US-09-054-832-10	Sequence 10, Appl
	18	3.6	90.0	6	3	US-09-346-290-48	Sequence 48, Appl
c	19	3.6	90.0	6	4	US-09-640-953-10	Sequence 10, Appl
	20	3.6	90.0	6	4	US-09-235-742-16	Sequence 16, Appl
c	21	3.6	90.0	6	4	US-09-235-742-16	Sequence 16, Appl
	22	3.6	90.0	6	4	US-09-347-343-21	Sequence 21, Appl
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	24	3.6	90.0	7	1	US-08-005-283-14	Sequence 14, Appl
	25	3.6	90.0	7	2	US-08-713-557B-7	Sequence 7, Appli
	26	3.6	90.0	7	2	US-08-442-809A-31	Sequence 31, Appl
	27	3.6	90.0	7	2	US-08-442-809A-35	Sequence 35, Appl
	28	3.6	90.0	7	3	US-08-641-291A-32	Sequence 32, Appl
	29	3.6	90.0	7	3	US-09-134-246-2	Sequence 2, Appli
	30	3.6	90.0	7	3	US-09-134-246-12	Sequence 12, Appl
	31	3.6	90.0	7	3	US-09-134-246-13	Sequence 13, Appl
	32	3.6	90.0	7	3	US-09-134-246-14	Sequence 14, Appl
	33	3.6	90.0	7	3	US-09-134-246-15	Sequence 15, Appl
	34	3.6	90.0	7	3	US-09-593-323-44	Sequence 44, Appl
	35	3.6	90.0	7	3	US-09-594-108-44	Sequence 44, Appl
	36	3.6	90.0	7	3	US-09-344-300-44	Sequence 44, Appl
c	37	3.6	90.0	7	3	US-09-632-538C-32	Sequence 32, Appl
	38	3.6	90.0	7	3	US-09-631-349A-14	Sequence 14, Appl
	39	3.6	90.0	7	3	US-09-313-221A-115	Sequence 115, App
c	40	3.6	90.0	7	3	US-09-313-221A-116	Sequence 116, App
	41	3.6	90.0	7	4	US-08-853-164C-3	Sequence 3, Appli
c	42	3.6	90.0	7	4	US-08-862-337-9	Sequence 9, Appli
c	43	3.6	90.0	7	4	US-09-968-733C-12	Sequence 12, Appl
c	44	3.6	90.0	7	4	US-09-968-733C-18	Sequence 18, Appl
	45	3.6	90.0	7	4	US-09-664-186-2	Sequence 2, Appli
	46	3.6	90.0	7	4	US-09-664-186-12	Sequence 12, Appl
	47	3.6	90.0	7	4	US-09-664-186-13	Sequence 13, Appl
	48	3.6	90.0	7	4	US-09-664-186-14	Sequence 14, Appl
	49	3.6	90.0	7	4	US-09-664-186-15	Sequence 15, Appl
	50	3.6	90.0	7	5	PCT-US94-08023-23	Sequence 23, Appl
	51	3.6	90.0	8	1	US-08-138-608-52	Sequence 52, Appl
c	52	3.6	90.0	8	1	US-08-105-483-423	Sequence 423, App
	53	3.6	90.0	8	1	US-08-242-409-11	Sequence 11, Appl
c	54	3.6	90.0	8	1	US-08-347-826A-13	Sequence 13, Appl
	55	3.6	90.0	8	1	US-07-882-838E-3	Sequence 3, Appli
	56	3.6	90.0	8	1	US-08-005-283-24	Sequence 24, Appl
	57	3.6	90.0	8	1	US-08-413-118-116	Sequence 116, App
	58	3.6	90.0	8	1	US-08-686-116A-8	Sequence 8, Appli
	59	3.6	90.0	8	1	US-08-685-484-8	Sequence 8, Appli
	60	3.6	90.0	8	1	US-08-847-108-8	Sequence 8, Appli
c	61	3.6	90.0	8	1	US-08-709-209-423	Sequence 423, App
c	62	3.6	90.0	8	1	US-08-303-275-131	Sequence 131, App
c	63	3.6	90.0	8	1	US-08-458-101-423	Sequence 423, App
	64	3.6	90.0	8	1	US-08-686-113A-21	Sequence 21, Appl
	65	3.6	90.0	8	1	US-08-717-526-72	Sequence 72, Appl
	66	3.6	90.0	8	1	US-08-847-095A-8	Sequence 8, Appli
c	67	3.6	90.0	8	1	US-08-410-779B-22	Sequence 22, Appl
c	68	3.6	90.0	8	2	US-08-466-337A-10	Sequence 10, Appl
	69	3.6	90.0	8	2	US-08-628-422-4	Sequence 4, Appli
c	70	3.6	90.0	8	2	US-08-475-359-10	Sequence 10, Appl
c	71	3.6	90.0	8	2	US-08-590-571-1	Sequence 1, Appli
c	72	3.6	90.0	8	2	US-08-590-571-4	Sequence 4, Appli
	73	3.6	90.0	8	3	US-08-836-022A-9	Sequence 9, Appli
c	74	3.6	90.0	8	3	US-08-465-887A-10	Sequence 10, Appl
	75	3.6	90.0	8	3	US-08-729-598-9	Sequence 9, Appli
	76	3.6	90.0	8	3	US-08-473-446-116	Sequence 116, App
c	77	3.6	90.0	8	3	US-08-962-790-4	Sequence 4, Appli
c	78	3.6	90.0	8	3	US-08-859-954-25	Sequence 25, Appl
	79	3.6	90.0	8	3	US-08-859-954-26	Sequence 26, Appl
	80	3.6	90.0	8	3	US-08-859-954-27	Sequence 27, Appl
	81	3.6	90.0	8	3	US-08-859-954-28	Sequence 28, Appl
c	82	3.6	90.0	8	3	US-08-859-954-56	Sequence 56, Appl
	83	3.6	90.0	8	3	US-08-859-954-80	Sequence 80, Appl
	84	3.6	90.0	8	3	US-08-859-954-81	Sequence 81, Appl
c	85	3.6	90.0	8	3	US-08-859-954-104	Sequence 104, App
c	86	3.6	90.0	8	3	US-08-859-954-105	Sequence 105, App
c	87	3.6	90.0	8	3	US-08-859-954-106	Sequence 106, App
c	88	3.6	90.0	8	3	US-08-859-954-107	Sequence 107, App
	89	3.6	90.0	8	3	US-08-859-954-127	Sequence 127, App
c	90	3.6	90.0	8	3	US-08-859-954-238	Sequence 238, App
c	91	3.6	90.0	8	3	US-08-859-954-332	Sequence 332, App
	92	3.6	90.0	8	3	US-08-859-954-333	Sequence 333, App
	93	3.6	90.0	8	3	US-08-859-954-334	Sequence 334, App
c	94	3.6	90.0	8	3	US-08-859-954-359	Sequence 359, App
c	95	3.6	90.0	8	3	US-08-859-954-360	Sequence 360, App
c	96	3.6	90.0	8	3	US-08-859-954-361	Sequence 361, App
	97	3.6	90.0	8	3	US-08-851-843A-44	Sequence 44, Appl
c	98	3.6	90.0	8	3	US-09-063-450-14	Sequence 14, Appl
c	99	3.6	90.0	8	3	US-09-063-450-16	Sequence 16, Appl
	100	3.6	90.0	8	3	US-09-063-450-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-08-973-568-54/c
; Sequence 54, Application US/08973568B
; Patent No. 6277634
; GENERAL INFORMATION:
;  APPLICANT: McCall, Maxine J.
;  APPLICANT: Hendry, Philip
;  APPLICANT: Lockett, Trevor
;  TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
;  FILE REFERENCE: 47203bpctus
;  CURRENT APPLICATION NUMBER: US/08/973,568B
;  CURRENT FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
;   OTHER INFORMATION: Synthetic Ribozyme or portion thereof
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
;   OTHER INFORMATION: portions thereof
US-08-973-568-54

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 3.7e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 1


RESULT 2
US-09-886-223-9
; Sequence 9, Application US/09886223
; Patent No. 6723513
; GENERAL INFORMATION:
;  APPLICANT: LEXOW, Preben
;  TITLE OF INVENTION: SEQUENCING METHOD USING MAGNIFYING TAGS
;  FILE REFERENCE: Q-64884
;  CURRENT APPLICATION NUMBER: US/09/886,223
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: PCT/GB99/04417
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: NO 19996339
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: NO 19996338
;  PRIOR FILING DATE: 1999-08-26
;  PRIOR APPLICATION NUMBER: NO 19996337
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: NO 19996336
;  PRIOR FILING DATE: 1999-06-11
;  PRIOR APPLICATION NUMBER: NO 19996335
;  PRIOR FILING DATE: 1999-04-19
;  PRIOR APPLICATION NUMBER: NO 19996334
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: NO 19996333
;  PRIOR FILING DATE: 1999-04-14
;  PRIOR APPLICATION NUMBER: NO 19996332
;  PRIOR FILING DATE: 1999-04-13
;  PRIOR APPLICATION NUMBER: NO 19996331
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: NO 19996330
;  PRIOR FILING DATE: 1999-02-26
;  PRIOR APPLICATION NUMBER: NO 19986133
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 4
;   TYPE: DNA
;   ORGANISM: synthetic construct
US-09-886-223-9

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 4;
  Best Local Similarity   25.0%;  Pred. No. 3.7e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 3
US-08-587-332B-11/c
; Sequence 11, Application US/08587332B
; Patent No. 5908745
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Lysov, Yuriy P
;    APPLICANT:  Yershov, Gennadiy M
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    TITLE OF INVENTION:  Use of Continuous/Contiguous Stacking
;    TITLE OF INVENTION:  Hybridization as a Diagnostic Tool.
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/587,332B
;      FILING DATE:  16-JAN-96
;    PRIOR APPLICATION DATA:  No. 5908745e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 5908745 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    FEATURE:
;      NAME/KEY:  No. 5908745e
;      LOCATION:  1-5
;      IDENTIFICATION METHOD:  Similarity with known sequences.
;      OTHER INFORMATION:  Nested primer of exons to a-thalassemia
;      OTHER INFORMATION:  gene.
US-08-587-332B-11

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 3e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 UUYG 4
              :::|
Db          4 TTCG 1


RESULT 4
US-08-855-372B-9/c
; Sequence 9, Application US/08855372B
; Patent No. 6090549
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous Stacking Hybridization as a Diagn
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/855,372B
;      FILING DATE:  13-MAY-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6090549 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-08-855-372B-9

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 3e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 5
US-09-498-851-9/c
; Sequence 9, Application US/09498851
; Patent No. 6440671
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous
;    TITLE OF INVENTION:  Stacking Hybridization as a Diagnostic Tool.
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/498,851
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/855,372
;      FILING DATE:  13-MAY-97
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6440671 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-09-498-851-9

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 3e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 6
US-08-683-045-10
; Sequence 10, Application US/08683045
; Patent No. 5652107
;  GENERAL INFORMATION:
;    APPLICANT:  Lizardi, Paul M.
;    APPLICANT:  Tyagi, Sanjay
;    APPLICANT:  Landegren, Ulf D.
;    APPLICANT:  Kramer, Fred R.
;    APPLICANT:  Szostak, Jack W.
;    TITLE OF INVENTION:  Diagnostic Assays and Kits for RNA Using
;    TITLE OF INVENTION:  RNA Binary Probes and a Ribozyme Ligase
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Davis Hoxie Faithfull & Hapgood
;      STREET:  45 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/683,045
;      FILING DATE:  15-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/315,191
;      FILING DATE:  29-SEP-1994
;      APPLICATION NUMBER:  US 08/005,893
;      FILING DATE:  15-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hone Esq., William J.
;      REGISTRATION NUMBER:  26,739
;      REFERENCE/DOCKET NUMBER:  11698.A39
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-757-2200
;      TELEFAX:  212-586-1461
;      TELEX:  421236
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
US-08-683-045-10

  Query Match             90.0%;  Score 3.6;  DB 1;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 7
US-08-393-888-17
; Sequence 17, Application US/08393888
; Patent No. 5759773
;  GENERAL INFORMATION:
;    APPLICANT:  Tyagi, Sanjay
;    APPLICANT:  Landegren, Ulf D.
;    APPLICANT:  Lizardi, Paul M.
;    APPLICANT:  Kramer, Fred R.
;    TITLE OF INVENTION:  SENSITIVE NUCLEIC ACID SANDWICH
;    TITLE OF INVENTION:  HYBRIDIZATION ASSAYS AND KITS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Davis Hoxie Faithfull & Hapgood
;      STREET:  45 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/393,888
;      FILING DATE:  24-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/006,073
;      FILING DATE:  15-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hone Esq., William J.
;      REGISTRATION NUMBER:  26,739
;      REFERENCE/DOCKET NUMBER:  11698.A38
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-757-2200
;      TELEFAX:  212-586-1461
;      TELEX:  421236
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-393-888-17

  Query Match             90.0%;  Score 3.6;  DB 1;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 8
US-08-463-288A-48
; Sequence 48, Application US/08463288A
; Patent No. 5820860
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine For Group B
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,288A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/363,311
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0609.2370007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-463-288A-48
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  Query Match             90.0%;  Score 3.6;  DB 1;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 9
US-08-470-445A-48
; Sequence 48, Application US/08470445A
; Patent No. 5843444
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine Against Group B
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,445A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/363,311
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0609.237000A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-470-445A-48

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 10
US-08-462-679-48
; Sequence 48, Application US/08462679
; Patent No. 5847081
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine For Group B
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,679
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/363,311
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0609.2370008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-462-679-48

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 11
US-08-466-210A-48
; Sequence 48, Application US/08466210A
; Patent No. 5858362
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine For Group B
```

```
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,210A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/363,311
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0609.237000B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-466-210A-48

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 12
US-08-485-158A-2
; Sequence 2, Application US/08485158A
; Patent No. 5859328
;  GENERAL INFORMATION:
;    APPLICANT:  Nasrallah, June B.
;    APPLICANT:  Nasrallah, Mikhail E.
;    APPLICANT:  Thorsness, Mary K.
;    TITLE OF INVENTION:  ISOLATED DNA ELEMENTS THAT DIRECT
;    TITLE OF INVENTION:  PISTIL-SPECIFIC AND ANTHER-SPECIFIC GENE EXPRESSION
;    TITLE OF INVENTION:  AND METHODS OF USING SAME
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak, & Seas
;      STREET:  2100 Pennsylania Avenue
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,158A
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mack, Susan J.
;      REGISTRATION NUMBER:  30,951
;      REFERENCE/DOCKET NUMBER:  A-6217-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-485-158A-2

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 13
US-08-467-147A-48
; Sequence 48, Application US/08467147A
; Patent No. 5908629
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine For Group B
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,147A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/363,311
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
```

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;      REFERENCE/DOCKET NUMBER:  0609.2370009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-467-147A-48

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 14
US-08-469-014-48
; Sequence 48, Application US/08469014
; Patent No. 5968521
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine Against Group B
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,014
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/363,311
;      FILING DATE:  22-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0609.2370006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-469-014-48

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 15
US-08-442-809A-12/c
; Sequence 12, Application US/08442809A
; Patent No. 5976873
;  GENERAL INFORMATION:
;    APPLICANT:  Bohinski, Robert J.,
;    APPLICANT:  Whitsett, Jeffrey A.
;    TITLE OF INVENTION:  Nucleic Acid Sequences
;    TITLE OF INVENTION:  Controlling Lung Cell -
;    TITLE OF INVENTION:  Specific Gene Expression
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,809A
;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,356
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  271010-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-08-442-809A-12

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTCG 2


RESULT 16
US-08-973-568-50/c
; Sequence 50, Application US/08973568B
; Patent No. 6277634
```

```
; GENERAL INFORMATION:
;  APPLICANT: McCall, Maxine J.
;  APPLICANT: Hendry, Philip
;  APPLICANT: Lockett, Trevor
;  TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
;  FILE REFERENCE: 47203bpctus
;  CURRENT APPLICATION NUMBER: US/08/973,568B
;  CURRENT FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
;   OTHER INFORMATION: Synthetic Ribozyme or portion thereof
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
;   OTHER INFORMATION: portions thereof
;   FEATURE:
;   NAME/KEY: misc_RNA
;   LOCATION: (1)
;   FEATURE:
;   NAME/KEY: misc_RNA
;   LOCATION: (6)
US-08-973-568-50

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTCG 2


RESULT 17
US-09-054-832-10/c
; Sequence 10, Application US/09054832
; Patent No. 6312894
;  GENERAL INFORMATION:
;    APPLICANT:  Meyer, Rich
;    TITLE OF INVENTION:  IMPROVED HYBRIDIZATION AND
;    TITLE OF INVENTION:  MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
;    TITLE OF INVENTION:  CONJUGATED TO MINOR GROOVE BINDERS
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/054,832
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,370
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brennan, Sean M
;      REGISTRATION NUMBER:  39,917
;      REFERENCE/DOCKET NUMBER:  34469-20004.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-054-832-10

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 3


RESULT 18
US-09-346-290-48
; Sequence 48, Application US/09346290
; Patent No. 6342223
;  GENERAL INFORMATION:
;    APPLICANT:  Michel, James L.
;    APPLICANT:  Kasper, Dennis L.
;    APPLICANT:  Ausubel, Frederick M.
;    APPLICANT:  Madoff, Lawrence C.
;    TITLE OF INVENTION:  Conjugate Vaccine Against Group B
;    TITLE OF INVENTION:  Streptococcus
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Avenue, NW, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/346,290
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/469,014
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,866
;      FILING DATE:  02-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/408,036
;      FILING DATE:  15-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0609.2370006
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;      TELEX:  248636 SSK
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-346-290-48

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 6;
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```
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 19
US-09-640-953-10/c
; Sequence 10, Application US/09640953
; Patent No. 6492346
;   GENERAL INFORMATION:
;        APPLICANT: Meyer, Rich
;        TITLE OF INVENTION: IMPROVED HYBRIDIZATION AND
;                            MISMATCH DISCRIMINATION USING OLIGONUCLEOTIDES
;                            CONJUGATED TO MINOR GROOVE BINDERS
;        NUMBER OF SEQUENCES: 40
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: PALO ALTO
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/640,953
;             FILING DATE: 16-Aug-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/054,832
;             FILING DATE: 03-APR-1998
;             APPLICATION NUMBER: 08/415,370
;             FILING DATE: 03-APR-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brennan, Sean M
;             REGISTRATION NUMBER: 39,917
;             REFERENCE/DOCKET NUMBER: 34469-20004.20
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-813-5600
;             TELEFAX: 650-494-0792
;             TELEX: 706141
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-640-953-10

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 3


RESULT 20
US-09-235-742-16
; Sequence 16, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  TITLE OF INVENTION: Immunization-Free Methods for Treating
;  TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
;  TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
;  TITLE OF INVENTION: Phenotype
;  FILE REFERENCE: 6510-170CON4
;  CURRENT APPLICATION NUMBER: US/09/235,742
;  CURRENT FILING DATE: 1999-01-21
;  EARLIER APPLICATION NUMBER: 08/927,120
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 08/593,554
;  EARLIER FILING DATE: 1996-01-30
;  EARLIER APPLICATION NUMBER: 08/725,968
;  EARLIER FILING DATE: 1996-10-04
;  EARLIER APPLICATION NUMBER: 60/028,118
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-16

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 21
US-09-235-742-16/c
; Sequence 16, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  TITLE OF INVENTION: Immunization-Free Methods for Treating
;  TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
;  TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
;  TITLE OF INVENTION: Phenotype
;  FILE REFERENCE: 6510-170CON4
;  CURRENT APPLICATION NUMBER: US/09/235,742
;  CURRENT FILING DATE: 1999-01-21
;  EARLIER APPLICATION NUMBER: 08/927,120
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 08/593,554
;  EARLIER FILING DATE: 1996-01-30
;  EARLIER APPLICATION NUMBER: 08/725,968
;  EARLIER FILING DATE: 1996-10-04
;  EARLIER APPLICATION NUMBER: 60/028,118
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-16

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 22
US-09-347-343-21
```

```
; Sequence 21, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT: KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/09/347,343A
;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-21

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 23
US-09-347-343-21/c
; Sequence 21, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT: KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/09/347,343A
;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 6
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-21

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 2.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 24
US-08-005-283-14
; Sequence 14, Application US/08005283
; Patent No. 5646261
;  GENERAL INFORMATION:
;    APPLICANT:  Uhlmann, Eugen
;    APPLICANT:  Peyman, Anuschirwan
;    APPLICANT:  O'Malley, Gerard
;    APPLICANT:  Helsberg, Matthias
;    APPLICANT:  Winkler, Irvin
;    TITLE OF INVENTION:  3'-Derivatized Oligonucleotide Analogs
;    TITLE OF INVENTION:  with No. 5646261-Nucleotidic Groupings, Their Preparation and
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/005,283
;      FILING DATE:  19-JAN-1993
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P4201663.0
;      FILING DATE:  22-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hammond, Alan W.
;      REGISTRATION NUMBER:  35,178
;      REFERENCE/DOCKET NUMBER:  02481.1270-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "The 5' end of SEQ ID
;      OTHER INFORMATION:  NO:14 is connected to the 5' end of SEQ ID
;      OTHER INFORMATION:  NO:15 by a (5'5'S) spacer. N is (5'5'S)G."
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  7
;      OTHER INFORMATION:  /note= "The 3'end of SEQ ID
;      OTHER INFORMATION:  NO:14 is connected to the 3' end of SEQ ID
;      OTHER INFORMATION:  NO:13 by a (3'3'S) spacer.  N is T(3'3'S)."
US-08-005-283-14

  Query Match             90.0%;  Score 3.6;  DB 1;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 25
US-08-713-557B-7
; Sequence 7, Application US/08713557B
; Patent No. 5912168
;  GENERAL INFORMATION:
;    APPLICANT:  Watson, James D.
;    APPLICANT:  Rudert, Fritz
;    TITLE OF INVENTION:  CD95 REGULATORY GENE SEQUENCES
;    TITLE OF INVENTION:  AND TRANSCRIPTION FACTORS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Ann W. Speckman
;      STREET:  2601 Elliott Avenue, Suite 4185
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/713,557B
;      FILING DATE:  30-AUG-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Speckman, Ann W
;      REGISTRATION NUMBER:  31,881
;      REFERENCE/DOCKET NUMBER:  11000.1004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-269-0565
;      TELEFAX:  206-269-0563
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-713-557B-7

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 26
US-08-442-809A-31
; Sequence 31, Application US/08442809A
; Patent No. 5976873
;  GENERAL INFORMATION:
;    APPLICANT:  Bohinski, Robert J.,
;    APPLICANT:  Whitsett, Jeffrey A.
;    TITLE OF INVENTION:  Nucleic Acid Sequences
;    TITLE OF INVENTION:  Controlling Lung Cell -
;    TITLE OF INVENTION:  Specific Gene Expression
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,809A
;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,356
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  271010-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-08-442-809A-31

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 27
US-08-442-809A-35
; Sequence 35, Application US/08442809A
; Patent No. 5976873
;  GENERAL INFORMATION:
;    APPLICANT:  Bohinski, Robert J.,
;    APPLICANT:  Whitsett, Jeffrey A.
;    TITLE OF INVENTION:  Nucleic Acid Sequences
;    TITLE OF INVENTION:  Controlling Lung Cell -
;    TITLE OF INVENTION:  Specific Gene Expression
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,809A
;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,356
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  271010-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-08-442-809A-35

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 28
US-08-641-291A-32
```

```
; Sequence 32, Application US/08641291A
; Patent No. 6037122
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT Claude
;    APPLICANT:  RUIMY Raymond
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERI
;    NUMBER OF SEQUENCES:  92
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oliff & Berridge
;      STREET:  700 South Washington Street, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IMB PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release  # 1.0, version  # 1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/641,291A
;      FILING DATE:  30-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Berridge, William P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38273
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6400
;      TELEFAX:  703-836-2787
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 base pairs
;      TYPE:  nucleotide
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
US-08-641-291A-32

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 2.1e+08;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              ||:|
Db          2 UUUG 5


RESULT 29
US-09-134-246-2
; Sequence 2, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
;  APPLICANT: Wayne, Jay
;  APPLICANT: Xu, Shuang-yong
;  TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
;  TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
;  TITLE OF INVENTION: Replication Origins
;  FILE REFERENCE: Thermus Shuttle Vector
;  CURRENT APPLICATION NUMBER: US/09/134,246B
;  CURRENT FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Thermus sp.
US-09-134-246-2

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 30
US-09-134-246-12
; Sequence 12, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
;  APPLICANT: Wayne, Jay
;  APPLICANT: Xu, Shuang-yong
;  TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
;  TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
;  TITLE OF INVENTION: Replication Origins
;  FILE REFERENCE: Thermus Shuttle Vector
;  CURRENT APPLICATION NUMBER: US/09/134,246B
;  CURRENT FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Thermus sp.
US-09-134-246-12

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 31
US-09-134-246-13
; Sequence 13, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
;  APPLICANT: Wayne, Jay
;  APPLICANT: Xu, Shuang-yong
;  TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
;  TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
;  TITLE OF INVENTION: Replication Origins
;  FILE REFERENCE: Thermus Shuttle Vector
;  CURRENT APPLICATION NUMBER: US/09/134,246B
;  CURRENT FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Thermus sp.
US-09-134-246-13

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 32
US-09-134-246-14
; Sequence 14, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
;  APPLICANT: Wayne, Jay
;  APPLICANT: Xu, Shuang-yong
;  TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
```

; TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-14

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 7

RESULT 33
US-09-134-246-15
; Sequence 15, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; APPLICANT: Xu, Shuang-yong
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-15

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 7

RESULT 34
US-09-593-323-44
; Sequence 44, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/593,323
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-44

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTCG 4

RESULT 35
US-09-594-108-44
; Sequence 44, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-44

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTCG 4

RESULT 36
US-09-344-300-44
; Sequence 44, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/344,300B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-344-300-44

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 37
US-09-632-538C-32/c
; Sequence 32, Application US/09632538C
; Patent No. 6440674
; GENERAL INFORMATION:
;  APPLICANT: Misra, Santosh et al.
;  TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
;  TITLE OF INVENTION:  ITS USE
;  FILE REFERENCE: 54359
;  CURRENT APPLICATION NUMBER: US/09/632,538C
;  CURRENT FILING DATE:  2000-08-04
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PROMOTER
;   OTHER INFORMATION: ELEMENTS
US-09-632-538C-32

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 38
US-09-631-349A-14
; Sequence 14, Application US/09631349A
; Patent No. 6455255
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Birkenmeyer, Larry G.
;  APPLICANT:  Leary, Thomas P.
;  APPLICANT:  Muerhoff, A. Scott
;  APPLICANT:  Desai, Suresh M.
;  APPLICANT:  Mushahwar, Isa K.
;  TITLE OF INVENTION: METHOD OF PERFORMING SUBTRACTIVE
;  TITLE OF INVENTION:  HYBRIDIZATION
;  FILE REFERENCE: 6714.US.01
;  CURRENT APPLICATION NUMBER: US/09/631,349A
;  CURRENT FILING DATE:  2000-08-02
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Linker/Adapter BE1R
US-09-631-349A-14

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 7


RESULT 39
```

```
US-09-313-221A-115
; Sequence 115, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
;  APPLICANT:  Thomas L. Romick (Inventor)
;  APPLICANT:  Mark S. Fraser (Inventor)
;  TITLE OF INVENTION:  PCR TECHNIQUES FOR DETECTING MICROBIAL
;  TITLE OF INVENTION:  AND VIRAL CONTAMINANTS IN FOODSTUFFS
;  FILE REFERENCE:  HUNT-042784
;  CURRENT APPLICATION NUMBER: US/09/313,221A
;  CURRENT FILING DATE:  1999-05-17
;  PRIOR APPLICATION NUMBER:  US 60/086,025
;  PRIOR FILING DATE:  1998-05-18
;  NUMBER OF SEQ ID NOS:  145
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 115
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Universal bacteria-specific nucleic acid sequence
US-09-313-221A-115

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 7


RESULT 40
US-09-313-221A-116/c
; Sequence 116, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
;  APPLICANT:  Thomas L. Romick (Inventor)
;  APPLICANT:  Mark S. Fraser (Inventor)
;  TITLE OF INVENTION:  PCR TECHNIQUES FOR DETECTING MICROBIAL
;  TITLE OF INVENTION:  AND VIRAL CONTAMINANTS IN FOODSTUFFS
;  FILE REFERENCE:  HUNT-042784
;  CURRENT APPLICATION NUMBER: US/09/313,221A
;  CURRENT FILING DATE:  1999-05-17
;  PRIOR APPLICATION NUMBER:  US 60/086,025
;  PRIOR FILING DATE:  1998-05-18
;  NUMBER OF SEQ ID NOS:  145
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 116
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Universal bacteria-specific nucleic acid sequence
US-09-313-221A-116

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 2.1e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 1


RESULT 41
US-08-853-164C-3
; Sequence 3, Application US/08853164C
; Patent No. 6489163
; GENERAL INFORMATION:
;  APPLICANT: Roy , Arun K.
;  APPLICANT:  Chen, Shuo
;  TITLE OF INVENTION: RIBOZYME MEDIATED INACTIVATION OF THE ANDROGEN RECEPTOR
```

; FILE REFERENCE: 4003.001500
; CURRENT APPLICATION NUMBER: US/08/853,164C
; CURRENT FILING DATE: 1997-05-08
; PRIOR APPLICATION NUMBER: 60/016,590
; PRIOR FILING DATE: 1996-05-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-08-853-164C-3

Query Match 90.0%; Score 3.6; DB 4; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 3 TTTG 6

RESULT 42
US-08-862-337-9/c
; Sequence 9, Application US/08862337
; Patent No. 6582902
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Kenan, Daniel J.
; APPLICANT: Tsai, Donald E.
; TITLE OF INVENTION: Nucleic Acid Epitopes and Methods of
; TITLE OF INVENTION: Making and Using the Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
; ADDRESSEE: Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 6582902th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,337
; FILING DATE: 23-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,196
; FILING DATE:
; APPLICATION NUMBER: US/07/956,693
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-69
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
US-08-862-337-9

Query Match 90.0%; Score 3.6; DB 4; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 43
US-09-968-733C-12/c
; Sequence 12, Application US/09968733C
; Patent No. 6773885
; GENERAL INFORMATION:
; APPLICANT: Walder, J
; APPLICANT: Behlke, M
; APPLICANT: Devor, E
; APPLICANT: Huang, L
; TITLE OF INVENTION: Compositions and Methods for Visual Ribonuclease Detection Assays
; FILE REFERENCE: 7614-019
; CURRENT APPLICATION NUMBER: US/09/968,733C
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/236,640
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric RNA Oligonucleotide
; OTHER INFORMATION: Substrate
; FEATURE:
; NAME/KEY: mod_base
; LOCATION: 1
; OTHER INFORMATION: n = 6-carboxyfluorescein
; FEATURE:
; NAME/KEY: mod_base
; LOCATION: 2, 6
; OTHER INFORMATION: a = 2'-O-methyl RNA base, adenosine
; FEATURE:
; NAME/KEY: mod_base
; LOCATION: 7
; OTHER INFORMATION: n = 4-(4'-dimethylaminophenylazo)benzoic acid
US-09-968-733C-12

Query Match 90.0%; Score 3.6; DB 4; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.1e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 6 TTCG 3

RESULT 44
US-09-968-733C-18/c
; Sequence 18, Application US/09968733C
; Patent No. 6773885
; GENERAL INFORMATION:
; APPLICANT: Walder, J
; APPLICANT: Behlke, M
; APPLICANT: Devor, E
; APPLICANT: Huang, L
; TITLE OF INVENTION: Compositions and Methods for Visual Ribonuclease Detection Assays
; FILE REFERENCE: 7614-019
; CURRENT APPLICATION NUMBER: US/09/968,733C
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/236,640

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;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 7
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Chimeric RNA Oligonucleotide
;   OTHER INFORMATION: Substrate
;   FEATURE:
;   NAME/KEY: mod_base
;   LOCATION: 1
;   OTHER INFORMATION: n = 6-carboxyfluorescein
;   FEATURE:
;   NAME/KEY: mod_base
;   LOCATION: 6
;   OTHER INFORMATION: a = 2'-O-methyl RNA base, adenosine
;   FEATURE:
;   NAME/KEY: mod_base
;   LOCATION: 7
;   OTHER INFORMATION: n = 4-(4'-dimethylaminophenylazo)benzoic acid
US-09-968-733C-18

  Query Match             90.0%;  Score 3.6;  DB 4;  Length 7;
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  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
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Db          6 TTCG 3


RESULT 45
US-09-664-186-2
; Sequence 2, Application US/09664186
; Patent No. 6815537
; GENERAL INFORMATION:
;  APPLICANT: Wayne, Jay
;  APPLICANT:  Xu, Shuang-yong
;  TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
;  TITLE OF INVENTION:  Vectors And Identification of Two Thermus Plasmid
;  TITLE OF INVENTION:  Replication Origins
;  FILE REFERENCE: Thermus Shuttle Vector
;  CURRENT APPLICATION NUMBER: US/09/664,186
;  CURRENT FILING DATE:  2000-09-18
;  PRIOR APPLICATION NUMBER: US/09/134,246B
;  PRIOR FILING DATE: 1998-08-14
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 7
;   TYPE: DNA
;   ORGANISM: Thermus sp.
US-09-664-186-2

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  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
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Db          4 TTTG 7


Search completed: April  4, 2005, 12:52:55
Job time : 99 secs
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 10:13:12 ; Search time 1436 Seconds
(without alignments)
134.973 Million cell updates/sec

Title: US-10-748-475-1
Perfect score: 4
Sequence: 1 uuyg 4

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	3.6	90.0	5	6	CQ787812	CQ787812 Sequence
	4	3.6	90.0	5	6	CQ787970	CQ787970 Sequence
c	5	3.6	90.0	5	6	CQ869002	CQ869002 Sequence
	6	3.6	90.0	5	6	CQ869003	CQ869003 Sequence
	7	3.6	90.0	5	6	CQ869005	CQ869005 Sequence
c	8	3.6	90.0	5	6	CQ869151	CQ869151 Sequence
	9	3.6	90.0	5	6	CQ869152	CQ869152 Sequence
	10	3.6	90.0	5	6	CQ869154	CQ869154 Sequence
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	12	3.6	90.0	5	6	AX103505	AX103505 Sequence
	13	3.6	90.0	5	6	AX103506	AX103506 Sequence
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	15	3.6	90.0	5	6	AX103522	AX103522 Sequence
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	17	3.6	90.0	5	6	AX155659	AX155659 Sequence
	18	3.6	90.0	5	6	AX155674	AX155674 Sequence
	19	3.6	90.0	5	6	AX155675	AX155675 Sequence
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c	21	3.6	90.0	6	6	BD228687	BD228687 Methods a
c	22	3.6	90.0	6	6	BD260030	BD260030 Hybridiza
	23	3.6	90.0	6	6	BD268081	BD268081 Cell spec
c	24	3.6	90.0	6	6	CQ755710	CQ755710 Sequence
c	25	3.6	90.0	6	6	CQ755798	CQ755798 Sequence
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c	27	3.6	90.0	6	6	CQ755838	CQ755838 Sequence
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c	32	3.6	90.0	6	6	CQ788027	CQ788027 Sequence
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	35	3.6	90.0	6	6	AX103536	AX103536 Sequence
	36	3.6	90.0	6	6	AX103537	AX103537 Sequence
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c	65	3.6	90.0	7	6	E65213	E65213 Method for
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	77	3.6	90.0	7	6	AX155720	AX155720 Sequence
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	80	3.6	90.0	7	6	AX155735	AX155735 Sequence
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	91	3.6	90.0	7	6	BD084747	BD084747 Human ner
	92	3.6	90.0	7	6	BD105929	BD105929 Leptospir

c 93	3.6	90.0	8	6	BD135593	BD135593	Observati
c 94	3.6	90.0	8	6	BD136069	BD136069	Novel pro
95	3.6	90.0	8	6	BD144670	BD144670	Peptide n
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c 98	3.6	90.0	8	6	BD193395	BD193395	Therapeut
99	3.6	90.0	8	6	BD205539	BD205539	Method of
100	3.6	90.0	8	6	BD205540	BD205540	Method of

ALIGNMENTS

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LOCUS BD230110 4 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for making complementary oligonucleotide tag sets.
ACCESSION BD230110
VERSION BD230110.1 GI:33039880
KEYWORDS JP 2002528137-A/27.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 4)
AUTHORS Williams,S.R., Kirchner,J.J. and Dubridge,R.B.
TITLE Method for making complementary oligonucleotide tag sets
JOURNAL Patent: JP 2002528137-A 27 03-SEP-2002;
LYNX THERAPEUTICS INC
COMMENT OS Artificial Sequence
PN JP 2002528137-A/27
PD 03-SEP-2002
PF 01-NOV-1999 JP 2000579783
PR 02-NOV-1998 US 60/106662
PI STEVEN R WILLIAMS,JAMES J KIRCHNER,ROBERT B DUBRIDGE PC
C12N15/09,C12N15/09,C12N11/00,C12Q1/68,C12N15/00,C12N15/00 CC
oligonucleotide
FH Key Location/Qualifiers
FT source 1. .4
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Query Match 90.0%; Score 3.6; DB 6; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.2e+10;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
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Db 4 TTTG 1

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LOCUS CQ787740 5 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 46 from Patent WO2004020664.
ACCESSION CQ787740
VERSION CQ787740.1 GI:45722698
KEYWORDS .
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 46 11-MAR-2004;
Universitaet Hohenheim (DE)
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repeat_unit 1. .5
/note="Anzahl der Wiederholungen: 4"
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Best Local Similarity 25.0%; Pred. No. 9.6e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
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Db 1 TTTG 4

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LOCUS CQ787812 5 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 118 from Patent WO2004020664.
ACCESSION CQ787812
VERSION CQ787812.1 GI:45722770
KEYWORDS .
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 118 11-MAR-2004;
Universitaet Hohenheim (DE)
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repeat_unit 1. .5
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ORIGIN

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Best Local Similarity 25.0%; Pred. No. 9.6e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTG 4

RESULT 4
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LOCUS CQ787970 5 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 276 from Patent WO2004020664.
ACCESSION CQ787970
VERSION CQ787970.1 GI:45722928
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes

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  JOURNAL   Patent: WO 2004020664-A 276 11-MAR-2004;
            Universitaet Hohenheim (DE)
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Qy          1 UUYG 4
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Db          1 TTTG 4


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DEFINITION  Sequence 156 from Patent WO2004074429.
ACCESSION   CQ869002
VERSION     CQ869002.1  GI:51998929
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   freskg Rd,P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
  TITLE     Method for producing second-generation library
  JOURNAL   Patent: WO 2004074429-A 156 02-SEP-2004;
            Nuevolution A/S (DK)
FEATURES             Location/Qualifiers
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Qy          1 UUYG 4
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Db          5 TTCG 2


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DEFINITION  Sequence 157 from Patent WO2004074429.
ACCESSION   CQ869003
VERSION     CQ869003.1  GI:51998930
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   freskg Rd,P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
  TITLE     Method for producing second-generation library
  JOURNAL   Patent: WO 2004074429-A 157 02-SEP-2004;
            Nuevolution A/S (DK)
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Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 7
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LOCUS       CQ869005                  5 bp    DNA     linear   PAT 13-SEP-2004
DEFINITION  Sequence 159 from Patent WO2004074429.
ACCESSION   CQ869005
VERSION     CQ869005.1  GI:51998932
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   freskg Rd,P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
  TITLE     Method for producing second-generation library
  JOURNAL   Patent: WO 2004074429-A 159 02-SEP-2004;
            Nuevolution A/S (DK)
FEATURES             Location/Qualifiers
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  Best Local Similarity   25.0%;  Pred. No. 9.6e+09;
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Qy          1 UUYG 4
              :::|
Db          2 TTCG 5


RESULT 8
CQ869151/c
LOCUS       CQ869151                  5 bp    DNA     linear   PAT 13-SEP-2004
DEFINITION  Sequence 305 from Patent WO2004074429.
ACCESSION   CQ869151
VERSION     CQ869151.1  GI:51999078
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   freskg Rd,P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
  TITLE     Method for producing second-generation library
  JOURNAL   Patent: WO 2004074429-A 305 02-SEP-2004;
            Nuevolution A/S (DK)
FEATURES             Location/Qualifiers
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Db          5 TTCG 2


RESULT 9
CQ869152
LOCUS       CQ869152                  5 bp    DNA     linear   PAT 13-SEP-2004
DEFINITION  Sequence 306 from Patent WO2004074429.
ACCESSION   CQ869152
VERSION     CQ869152.1  GI:51999079
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   freskg Rd,P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
  TITLE     Method for producing second-generation library
  JOURNAL   Patent: WO 2004074429-A 306 02-SEP-2004;
            Nuevolution A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 10
CQ869154
LOCUS       CQ869154                  5 bp    DNA     linear   PAT 13-SEP-2004
DEFINITION  Sequence 308 from Patent WO2004074429.
ACCESSION   CQ869154
VERSION     CQ869154.1  GI:51999081
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   freskg Rd,P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
  TITLE     Method for producing second-generation library
  JOURNAL   Patent: WO 2004074429-A 308 02-SEP-2004;
            Nuevolution A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTCG 5


RESULT 11
AX098547/c
LOCUS       AX098547                  5 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 5 from Patent WO0119792.
ACCESSION   AX098547
VERSION     AX098547.1  GI:13537811
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Turin,L.M., Pitt,A.R., Suckling,C.J. and Waigh,R.D.
  TITLE     Covalently linked dimeric dna binding molecules
  JOURNAL   Patent: WO 0119792-A 5 22-MAR-2001;
            GENELABS TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 12
AX103505
LOCUS       AX103505                  5 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 70 from Patent EP1104811.
ACCESSION   AX103505
VERSION     AX103505.1  GI:13919773
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 70 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 13
AX103506
LOCUS       AX103506                  5 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 71 from Patent EP1104811.
ACCESSION   AX103506
VERSION     AX103506.1  GI:13919774
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 71 06-JUN-2001;
            INNOGENETICS N.V. (BE)
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FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 14
AX103521
LOCUS       AX103521                  5 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 86 from Patent EP1104811.
ACCESSION   AX103521
VERSION     AX103521.1  GI:13919789
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 86 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 15
AX103522
LOCUS       AX103522                  5 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 87 from Patent EP1104811.
ACCESSION   AX103522
VERSION     AX103522.1  GI:13919790
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 87 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 16
AX155658
LOCUS       AX155658                  5 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 70 from Patent WO0140279.
ACCESSION   AX155658
VERSION     AX155658.1  GI:14536856
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 70 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 17
AX155659
LOCUS       AX155659                  5 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 71 from Patent WO0140279.
ACCESSION   AX155659
VERSION     AX155659.1  GI:14536857
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 71 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity  25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 18
AX155674
LOCUS       AX155674                  5 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 86 from Patent WO0140279.
ACCESSION   AX155674
VERSION     AX155674.1  GI:14536872
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KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 86 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 19
AX155675
LOCUS       AX155675                  5 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 87 from Patent WO0140279.
ACCESSION   AX155675
VERSION     AX155675.1  GI:14536873
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 87 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 9.6e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 20
BD228687
LOCUS       BD228687                  6 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and adjuvants for stimulating mucosal immunity.
ACCESSION   BD228687
VERSION     BD228687.1  GI:33038457
KEYWORDS    JP 2002526425-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Raz,E., Horner,A.A. and Carson,D.A.
  TITLE     Methods and adjuvants for stimulating mucosal immunity
  JOURNAL   Patent: JP 2002526425-A 16 20-AUG-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002526425-A/16
            PD   20-AUG-2002
            PF   15-SEP-1999 JP 2000573397
            PR   05-OCT-1998 US    09/167039
            PI   EYAL RAZ,ANTHONY A HORNER,DENNIS A CARSON
            PC   A61K39/39,A61K31/7088,A61K31/7105,A61K31/711,A61P11/00 PC
            ,A61P27/14,A61P37/04,
            PC   C12N15/09,G01N33/15,G01N33/50//C12N5/10,G01N33/531,C12N15/00,
            PC   C12N5/00
            CC   non-coding oligonucleotides
            FH   Key             Location/Qualifiers
            FT   source          1. .6
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 21
BD228687/c
LOCUS       BD228687                  6 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and adjuvants for stimulating mucosal immunity.
ACCESSION   BD228687
VERSION     BD228687.1  GI:33038457
KEYWORDS    JP 2002526425-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Raz,E., Horner,A.A. and Carson,D.A.
  TITLE     Methods and adjuvants for stimulating mucosal immunity
  JOURNAL   Patent: JP 2002526425-A 16 20-AUG-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002526425-A/16
            PD   20-AUG-2002
            PF   15-SEP-1999 JP 2000573397
            PR   05-OCT-1998 US    09/167039
            PI   EYAL RAZ,ANTHONY A HORNER,DENNIS A CARSON
            PC   A61K39/39,A61K31/7088,A61K31/7105,A61K31/711,A61P11/00 PC
            ,A61P27/14,A61P37/04,
            PC   C12N15/09,G01N33/15,G01N33/50//C12N5/10,G01N33/531,C12N15/00,
            PC   C12N5/00
            CC   non-coding oligonucleotides
            FH   Key             Location/Qualifiers
            FT   source          1. .6
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3
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RESULT 22
BD260030/c
LOCUS       BD260030                  6 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders.
ACCESSION   BD260030
VERSION     BD260030.1  GI:33069800
KEYWORDS    JP 2002527040-A/10.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Hedgpeth,J., Afonina,I.A., Kutyavin,I.V., Lukhtanov,E.A.,
            Belousov,E.S. and Jr,R.B.M.
  TITLE     Hybridization and mismatch discrimination using oligonucleotides
            conjugated to minor groove binders
  JOURNAL   Patent: JP 2002527040-A 10 27-AUG-2002;
            EPOCH BIOSCIENCES INC
COMMENT     OS   Escherichia coli
            PN   JP 2002527040-A/10
            PD   27-AUG-2002
            PF   05-APR-1999 JP 2000542342
            PR   03-APR-1998 US    09/054832
            PI   JOEL HEDGPETH,IRINA A AFONINA,IGOR V KUTYAVIN,EUGENY A  PI
            LUKHTANOV,
            PI   EVGENIY S BELOUSOV,RICH B MEYER JR
            PC   C12N15/09,C12N15/09,C07H21/02,C07H21/04,C12Q1/68,G01N21/78, PC
              G01N33/483,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N15/00
            CC   Hybridization and mismatch discrimination using  CC
            oligonucleotides
            CC   conjugated to minor groove binders
            FH   Key             Location/Qualifiers
            FT   source          1. .6
            FT                   /organism='Escherichia coli'.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 3


RESULT 23
BD268081
LOCUS       BD268081                  6 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Cell specific promoters of uncoupling protein 3.
ACCESSION   BD268081
VERSION     BD268081.1  GI:33077849
KEYWORDS    JP 2002534057-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Esterbauer,H., Oberkofler,H. and Patsch,W.
  TITLE     Cell specific promoters of uncoupling protein 3
  JOURNAL   Patent: JP 2002534057-A 8 15-OCT-2002;
            BOEHRINGER INGELHEIM INTERNATIONAL GMBH
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534057-A/8
            PD   15-OCT-2002
            PF   21-AUG-1999 JP 2000567683
            PR   27-AUG-1998 DE 198 38 837.3
            PI   HARALD ESTERBAUER,HANNES OBERKOFLER,WOLFGANG PATSCH PC
            C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/ PC
            66,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,G01N37/00,C12N15/00,C12N5/00 CC
              E-Box
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(6).
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 24
CQ755710/c
LOCUS       CQ755710                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 211 from Patent WO2003106674.
ACCESSION   CQ755710
VERSION     CQ755710.1  GI:44846515
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE     Means and methods for regulating gene expression
  JOURNAL   Patent: WO 2003106674-A 211 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTCG 2


RESULT 25
CQ755798/c
LOCUS       CQ755798                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 299 from Patent WO2003106674.
ACCESSION   CQ755798
VERSION     CQ755798.1  GI:44846603
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE     Means and methods for regulating gene expression
  JOURNAL   Patent: WO 2003106674-A 299 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 26
CQ755827
LOCUS       CQ755827                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 328 from Patent WO2003106674.
ACCESSION   CQ755827
VERSION     CQ755827.1  GI:44846632
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE     Means and methods for regulating gene expression
  JOURNAL   Patent: WO 2003106674-A 328 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 27
CQ755838/c
LOCUS       CQ755838                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 339 from Patent WO2003106674.
ACCESSION   CQ755838
VERSION     CQ755838.1  GI:44846643
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE     Means and methods for regulating gene expression
  JOURNAL   Patent: WO 2003106674-A 339 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 28
CQ757948/c
LOCUS       CQ757948                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 252 from Patent WO2003106684.
ACCESSION   CQ757948
VERSION     CQ757948.1  GI:44847969
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
  TITLE     A method for the stimultaneaous production of multiple proteins;
            vectors and cells for use therein
  JOURNAL   Patent: WO 2003106684-A 252 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTCG 2


RESULT 29
CQ758036/c
LOCUS       CQ758036                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 340 from Patent WO2003106684.
ACCESSION   CQ758036
VERSION     CQ758036.1  GI:44848057
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
  TITLE     A method for the stimultaneaous production of multiple proteins;
            vectors and cells for use therein
  JOURNAL   Patent: WO 2003106684-A 340 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
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```
              :::|
Db          6 TTCG 3


RESULT 30
CQ758065
LOCUS       CQ758065                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 369 from Patent WO2003106684.
ACCESSION   CQ758065
VERSION     CQ758065.1  GI:44848086
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
  TITLE     A method for the stimultaneaous production of multiple proteins;
            vectors and cells for use therein
  JOURNAL   Patent: WO 2003106684-A 369 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 31
CQ758076/c
LOCUS       CQ758076                  6 bp    DNA     linear   PAT 01-MAR-2004
DEFINITION  Sequence 380 from Patent WO2003106684.
ACCESSION   CQ758076
VERSION     CQ758076.1  GI:44848097
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
  TITLE     A method for the stimultaneaous production of multiple proteins;
            vectors and cells for use therein
  JOURNAL   Patent: WO 2003106684-A 380 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide patterns over-represented in STAR
                     elements"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 32
CQ788027/c
LOCUS       CQ788027                  6 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 333 from Patent WO2004020664.
ACCESSION   CQ788027
VERSION     CQ788027.1  GI:45722983
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Geldermann,H., Preuss,S. and Han,Y.
  TITLE     Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
  JOURNAL   Patent: WO 2004020664-A 333 11-MAR-2004;
            Universitaet Hohenheim (DE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     satellite       1. .6
                     /note="M05, Allel R (PrP-Gen)"
     repeat_unit     1. .2
                     /note="Anzahl der Wiederholungen: 2"
     repeat_unit     5. .6
                     /note="Anzahl der Wiederholungen: 2"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 33
CQ801401
LOCUS       CQ801401                  6 bp    DNA     linear   PAT 05-MAY-2004
DEFINITION  Sequence 14 from Patent WO2004032958.
ACCESSION   CQ801401
VERSION     CQ801401.1  GI:47058062
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Pizza,M.C.
  TITLE     Polypeptide-vaccines for broad protection against hypervirulent
            meningococcal lineages
  JOURNAL   Patent: WO 2004032958-A 14 22-APR-2004;
            Chiron SRL (IT)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="CpG motif"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 34
E17073
```

```
LOCUS       E17073                    6 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Fusarium sp. - specific sequence in 18S rRNA gene.
ACCESSION   E17073
VERSION     E17073.1  GI:5711756
KEYWORDS    JP 1998234380-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Shibata,Y., Takashina,T., Shindo,Y. and Takahashi,I.
  TITLE     NUCLEIC ACID SEQUENCE FOR DETECTING FUNGUS OF GENUS FUSARIUM
  JOURNAL   Patent: JP 1998234380-A 2 08-SEP-1998;
            SHINKINRUI KINOU KAIHATSU KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1998234380-A/2
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062104
            PI   SHIBATA YOSHIKAZU, TAKASHINA TOMONORI, SHINDO YOSHIO, PI
            TAKAHASHI ISAMU
            PC   C12N15/09,C07H21/04,C12Q1/68//C12N1/14,(C12N15/09,C12R1:77),
            PC   (C12Q1/68,
            PC   C12R1:77),(C12N1/14,C12R1:77);
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .6
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 35
AX103536
LOCUS       AX103536                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 101 from Patent EP1104811.
ACCESSION   AX103536
VERSION     AX103536.1  GI:13919804
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 101 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 36
AX103537
LOCUS       AX103537                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 102 from Patent EP1104811.
ACCESSION   AX103537
VERSION     AX103537.1  GI:13919805
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 102 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 37
AX103538
LOCUS       AX103538                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 103 from Patent EP1104811.
ACCESSION   AX103538
VERSION     AX103538.1  GI:13919806
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 103 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 38
AX103552
LOCUS       AX103552                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 117 from Patent EP1104811.
ACCESSION   AX103552
VERSION     AX103552.1  GI:13919820
KEYWORDS    .
SOURCE      Hepatitis B virus
```

```
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 117 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 39
AX103553
LOCUS       AX103553                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 118 from Patent EP1104811.
ACCESSION   AX103553
VERSION     AX103553.1  GI:13919821
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 118 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 40
AX103554
LOCUS       AX103554                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 119 from Patent EP1104811.
ACCESSION   AX103554
VERSION     AX103554.1  GI:13919822
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L.
  TITLE     Hbv sequences
  JOURNAL   Patent: EP 1104811-A 119 06-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

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  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 41
AX104454
LOCUS       AX104454                  6 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 646 from Patent WO0122972.
ACCESSION   AX104454
VERSION     AX104454.1  GI:13920651
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 646 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 42
AX155689
LOCUS       AX155689                  6 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 101 from Patent WO0140279.
ACCESSION   AX155689
VERSION     AX155689.1  GI:14536887
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 101 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6
```

```
RESULT 43
AX155690
LOCUS       AX155690                  6 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 102 from Patent WO0140279.
ACCESSION   AX155690
VERSION     AX155690.1  GI:14536888
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 102 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 44
AX155691
LOCUS       AX155691                  6 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 103 from Patent WO0140279.
ACCESSION   AX155691
VERSION     AX155691.1  GI:14536889
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 103 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 45
AX155705
LOCUS       AX155705                  6 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 117 from Patent WO0140279.
ACCESSION   AX155705
VERSION     AX155705.1  GI:14536903
KEYWORDS    .
SOURCE      Hepatitis B virus
  ORGANISM  Hepatitis B virus
            Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Stuyver,L., van Geyt,C. and de Gendt,S.
  TITLE     New hbv sequences
  JOURNAL   Patent: WO 0140279-A 117 07-JUN-2001;
            INNOGENETICS N.V. (BE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Hepatitis B virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10407"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


Search completed: April  4, 2005, 12:17:13
Job time : 1443 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 09:25:09 ; Search time 278 Seconds
(without alignments)
85.176 Million cell updates/sec

Title: US-10-748-475-1
Perfect score: 4
Sequence: 1 uuyg 4

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	3.6	90.0	5	2	AAV72348	Aav72348 US5908745
	2	3.6	90.0	6	2	AAQ78699	Aaq78699 Pistil ge
	3	3.6	90.0	6	2	AAT80316	Aat80316 Oligo HCV
	4	3.6	90.0	6	2	AAV61658	Aav61658 Fusarium
	5	3.6	90.0	6	3	AAZ89328	Aaz89328 Human UCP
	6	3.6	90.0	6	6	ABS78162	Abs78162 Angiogene
c	7	3.6	90.0	6	6	ABN73675	Abn73675 Bovine em
	8	3.6	90.0	6	6	ABS65900	Abs65900 Inhibitor
c	9	3.6	90.0	6	6	ABK30086	Abk30086 Beta-lact
	10	3.6	90.0	6	9	ACD99934	Acd99934 Immunosti
c	11	3.6	90.0	6	9	ACH50857	Ach50857 Hypotheti
c	12	3.6	90.0	6	9	ACH50858	Ach50858 Hypotheti
c	13	3.6	90.0	6	9	ACH50860	Ach50860 Hypotheti
c	14	3.6	90.0	6	9	ACH50845	Ach50845 Hypotheti
c	15	3.6	90.0	6	9	ACH50859	Ach50859 Hypotheti
c	16	3.6	90.0	6	9	ACH50850	Ach50850 Hypotheti
c	17	3.6	90.0	6	9	ACH50849	Ach50849 Hypotheti
c	18	3.6	90.0	6	9	ACH50851	Ach50851 Hypotheti
c	19	3.6	90.0	6	9	ACH50848	Ach50848 Hypotheti
c	20	3.6	90.0	6	9	ACH50843	Ach50843 Hypotheti
c	21	3.6	90.0	6	13	ADR33065	Adr33065 Human nic
c	22	3.6	90.0	6	13	ADR33243	Adr33243 Human nic
c	23	3.6	90.0	6	13	ADR33006	Adr33006 Human nic
c	24	3.6	90.0	6	13	ADR33007	Adr33007 Human nic
	25	3.6	90.0	6	13	ADR32753	Adr32753 Human nic
c	26	3.6	90.0	6	13	ADR33260	Adr33260 Human nic
	27	3.6	90.0	6	13	ADR32558	Adr32558 Human nic
c	28	3.6	90.0	7	2	AAQ45285	Aaq45285 Sequence
	29	3.6	90.0	7	2	AAT75839	Aat75839 Corynebac
	30	3.6	90.0	7	2	AAV58899	Aav58899 Leptospir
	31	3.6	90.0	7	3	AAA27964	Aaa27964 Box W1 we
	32	3.6	90.0	7	3	AAZ48430	Aaz48430 Bacteria
c	33	3.6	90.0	7	3	AAZ48459	Aaz48459 Nucleic a
	34	3.6	90.0	7	6	AAD32130	Aad32130 Linker/Ad
c	35	3.6	90.0	7	6	ABK88715	Abk88715 Human CD9
	36	3.6	90.0	7	6	ABK88705	Abk88705 Human CD9
	37	3.6	90.0	7	8	ACD56778	Acd56778 Synthetic
	38	3.6	90.0	7	8	ACD56769	Acd56769 Synthetic
	39	3.6	90.0	7	9	ADA36984	Ada36984 RNA oligo
c	40	3.6	90.0	7	10	ADH76936	Adh76936 DNA motif
	41	3.6	90.0	7	13	ADR36886	Adr36886 Human nic
c	42	3.6	90.0	7	13	ADR33128	Adr33128 Human nic
	43	3.6	90.0	7	13	ADR36888	Adr36888 Human nic
	44	3.6	90.0	7	13	ADR36887	Adr36887 Human nic
	45	3.6	90.0	7	13	ADR36885	Adr36885 Human nic
	46	3.6	90.0	7	13	ADR42914	Adr42914 T cell fa
c	47	3.6	90.0	8	1	AAN90803	Aan90803 Sequence
c	48	3.6	90.0	8	1	AAN90805	Aan90805 Sequence
c	49	3.6	90.0	8	2	AAQ31554	Aaq31554 Oct-1 pro
	50	3.6	90.0	8	2	AAQ66132	Aaq66132 Hairpin l
c	51	3.6	90.0	8	2	AAQ66131	Aaq66131 Hairpin l
	52	3.6	90.0	8	2	AAQ97979	Aaq97979 Peptide n
c	53	3.6	90.0	8	2	AAQ97970	Aaq97970 Peptide n
c	54	3.6	90.0	8	2	AAT14136	Aat14136 Cytokine
	55	3.6	90.0	8	2	AAT27564	Aat27564 Adenoviru
c	56	3.6	90.0	8	2	AAT13824	Aat13824 Carnation
c	57	3.6	90.0	8	2	AAT75496	Aat75496 P. americ
c	58	3.6	90.0	8	2	AAV56863	Aav56863 Regulator
	59	3.6	90.0	8	2	AAV11192	Aav11192 Peptide n
	60	3.6	90.0	8	2	AAX29655	Aax29655 Primer fo
c	61	3.6	90.0	8	3	AAZ93600	Aaz93600 Cell cycl
c	62	3.6	90.0	8	3	AAA11726	Aaa11726 Human pro
	63	3.6	90.0	8	3	AAA10327	Aaa10327 DNA ligan
c	64	3.6	90.0	8	3	AAA14120	Aaa14120 E. coli K
	65	3.6	90.0	8	3	AAA14143	Aaa14143 E. coli K
	66	3.6	90.0	8	3	AAA81021	Aaa81021 A. thalia
	67	3.6	90.0	8	3	AAA80768	Aaa80768 A. thalia
	68	3.6	90.0	8	3	AAA80713	Aaa80713 A. thalia
	69	3.6	90.0	8	3	AAA80714	Aaa80714 A. thalia
	70	3.6	90.0	8	3	AAA80715	Aaa80715 A. thalia
c	71	3.6	90.0	8	3	AAA80925	Aaa80925 A. thalia
c	72	3.6	90.0	8	3	AAA81046	Aaa81046 A. thalia
c	73	3.6	90.0	8	3	AAA81048	Aaa81048 A. thalia
c	74	3.6	90.0	8	3	AAA80712	Aaa80712 A. thalia
c	75	3.6	90.0	8	3	AAA80743	Aaa80743 A. thalia
	76	3.6	90.0	8	3	AAA81020	Aaa81020 A. thalia
c	77	3.6	90.0	8	3	AAA80792	Aaa80792 A. thalia
c	78	3.6	90.0	8	3	AAA80794	Aaa80794 A. thalia
c	79	3.6	90.0	8	3	AAA81047	Aaa81047 A. thalia
c	80	3.6	90.0	8	3	AAA80791	Aaa80791 A. thalia
c	81	3.6	90.0	8	3	AAA81019	Aaa81019 A. thalia
	82	3.6	90.0	8	3	AAA80814	Aaa80814 A. thalia
c	83	3.6	90.0	8	3	AAA80793	Aaa80793 A. thalia
	84	3.6	90.0	8	3	AAA80767	Aaa80767 A. thalia
	85	3.6	90.0	8	3	AAA47694	Aaa47694 Transcrip
	86	3.6	90.0	8	3	AAA47692	Aaa47692 Transcrip
	87	3.6	90.0	8	3	AAA47696	Aaa47696 Human cyc
	88	3.6	90.0	8	4	AAA92376	Aaa92376 CG motif
c	89	3.6	90.0	8	4	AAA92376	Aaa92376 CG motif
c	90	3.6	90.0	8	6	ABS54040	Abs54040 Feline im
	91	3.6	90.0	8	6	ABS78215	Abs78215 Angiogene
	92	3.6	90.0	8	6	ABS78143	Abs78143 Angiogene
c	93	3.6	90.0	8	6	ABS78187	Abs78187 Angiogene

	94	3.6	90.0	8	6	ABS78306	Abs78306 Angiogene
c	95	3.6	90.0	8	6	ABS78306	Abs78306 Angiogene
c	96	3.6	90.0	8	6	ABS78185	Abs78185 Angiogene
	97	3.6	90.0	8	6	AAL39241	Aal39241 Murine To
c	98	3.6	90.0	8	6	AAL39241	Aal39241 Murine To
	99	3.6	90.0	8	6	ABS70541	Abs70541 Dendritic
c	100	3.6	90.0	8	6	ABS70541	Abs70541 Dendritic

ALIGNMENTS

RESULT 1
AAV72348/c
ID AAV72348 standard; DNA; 5 BP.
XX
AC AAV72348;
XX
DT 28-JUL-1999 (first entry)
XX
DE US5908745 primer #5.
XX
KW DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW continuous/contiguous stacking hybridization technique; detection;
KW mutation; diagnosis; primer; ss.
XX
OS Synthetic.
XX
PN US5908745-A.
XX
PD 01-JUN-1999.
XX
PF 16-JAN-1996; 96US-00587332.
XX
PR 16-JAN-1996; 96US-00587332.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Yershov GM, Barski VE, Lysov YP, Mirzabekov AD, Kirillov EV;
PI Parinov SV;
XX
DR WPI; 1999-347002/29.
XX
PT Detecting disease-associated alleles using continuous/contiguous stacking
PT hybridization as a diagnostic tool.
XX
PS Example 1; Col 9; 16pp; English.
XX
CC This invention describes novel methods for sequencing and analysing DNA
CC samples to detect disease-associated alleles, by continuous/contiguous
CC stacking hybridization techniques (utilizing universal bases) with
CC oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC be used to detect multiple DNA base mutations which are specific for
CC certain diseases. The methods of the invention provide accurate and
CC efficient and sensitive methods for diagnosing disease by detecting
CC multiple mutation sequences in patient DNA. The method require the
CC minimum number of oligonucleotides and few stacking hybridization steps
CC than prior art methods. The methods are also efficient enough to
CC discriminate between perfect and imperfect duplexes. The methods also
CC obviate the need for the fabrication and array placement of large numbers
CC of immobilized oligomers
XX
SQ Sequence 5 BP; 2 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 1.1e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 UUYG 4
              :::|
Db          4 TTCG 1
```

RESULT 2
AAQ78699
ID AAQ78699 standard; DNA; 6 BP.
XX
AC AAQ78699;
XX
DT 25-MAR-2003 (revised)
DT 06-JUN-1995 (first entry)
XX
DE Pistil gene promoter consensus sequence.
XX
KW Pistil; anther; gene expression; female sterile; male sterile;
KW S-locus glycoprotein; SLG; S-locus related gene; SLR1; promoter;
KW transgenic plant; crop improvement; ds.
XX
OS Brassica sp.
XX
PN WO9425613-A1.
XX
PD 10-NOV-1994.
XX
PF 03-MAY-1994; 94WO-US004557.
XX
PR 03-MAY-1993; 93US-00054362.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Nasrallah ME, Nasrallah JB, Thorsness MK;
XX
DR WPI; 1994-358288/44.
XX
PT Isolated DNA elements directing pistil- or anther-specific gene
PT expression - used to cause female and male sterility in plants.
XX
PS Disclosure; Page 32; 54pp; English.
XX
CC Comparison of the promoter regions of Brassica sp. S-locus glycoprotein
CC SLG13, SLG2, SLG8 and S-locus related SLR1 genes (given in AAQ78703-06)
CC identified consensus sequences, which can be used as minimal promoter
CC elements for pistil- or anther-specific gene expression in plants. The
CC pistil-specific element has at least 70% homology to the consensus
CC elements given in AAQ78698-700. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 6 BP; 0 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 2; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 UUYG 4
              :::|
Db          2 TTTG 5
```

RESULT 3
AAT80316
ID AAT80316 standard; DNA; 6 BP.
XX
AC AAT80316;
XX
DT 16-OCT-1997 (first entry)
XX
DE Oligo HCV-204, targetted to HCV mRNA position +20 to +25.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .6

```
FT                  /*tag= a
FT                  /note= "Comprises phosphorothioate linkages"
XX
PN   WO9639500-A2.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP002427.
XX
PR   06-JUN-1995;   95US-00471968.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Frank BL,  Goodchild J,  Hamlin HA,  Kilkuskie RE,  Roberts NA;
PI   Roberts PC,  Walther DM,  Wolfe JL;
XX
DR   WPI; 1997-043122/04.
XX
PT   Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT   the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT   carcinoma.
XX
PS   Claim 1; Page 17; 100pp; English.
XX
CC   The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC   which are complementary to a portion of the 5' untranslated region (UTR)
CC   of hepatitis C virus (HCV). These sequences may be used in a
CC   pharmaceutical composition for the control or prevention of HCV
CC   infection. They may be used to inhibit replication or expression of HCV
CC   or for detecting the presence of HCV in a sample. They may be used to
CC   inhibit HCV replication in a cell and are therefor useful in the
CC   treatment of HCV infections such as chronic and acute hepatitis and
CC   hepatocarcinoma
XX
SQ   Sequence 6 BP; 1 A; 0 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 4
AAV61658
ID   AAV61658 standard; DNA; 6 BP.
XX
AC   AAV61658;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Fusarium sp. 18S rRNA DNA fragment #2.
XX
KW   18S rRNA; detection; identification; fungus; ss.
XX
OS   Fusarium sp.
XX
PN   JP10234380-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062104.
XX
PR   28-FEB-1997;   97JP-00062104.
XX
PA   (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX
DR   WPI; 1998-535034/46.
XX
PT   Use of oligo:nucleotide for detecting and identification of fungus of
PT   Fusarium genus - as primer or probe to detect of identify microbes
PT   rapidly and exactly.
XX
PS   Claim 1; Page 6; 20pp; Japanese.
XX
CC   AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
CC   used in a method for the detection and identification of a fungus of
CC   Fusarium genus. The process can be used to detect or identify microbes
CC   rapidly and exactly
XX
SQ   Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 5
AAZ89328
ID   AAZ89328 standard; DNA; 6 BP.
XX
AC   AAZ89328;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human UCP3 promoter fragment #8.
XX
KW   UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KW   fat metabolism; ss.
XX
OS   Homo sapiens.
XX
PN   DE19838837-A1.
XX
PD   02-MAR-2000.
XX
PF   27-AUG-1998;   98DE-01038837.
XX
PR   27-AUG-1998;   98DE-01038837.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Esterbauer H,  Oberkofler H,  Patsch W;
XX
DR   WPI; 2000-272214/24.
XX
PT   Recombinant fat and muscle tissue specific uncoupling protein 3 promoters
PT   useful for identifying UCP3 modulators.
XX
PS   Claim 19; Page 11; 38pp; German.
XX
CC   This invention describes novel recombinant DNA molecules containing an
CC   uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat cells
CC   but not functional in muscle cells or vice versa. The recombinant DNA
CC   molecules are useful for transcription of genes and, with host cells, to
CC   test for substances that can influence transcription. They can also be
CC   used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC   metabolism and control of the promoter is useful in combating diseases
CC   with inappropriate fat tissue metabolism. This sequence represents a
CC   fragment of the human UCP-3 promoter which is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 6 BP; 1 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 6
ABS78162
ID   ABS78162 standard; DNA; 6 BP.
XX
AC   ABS78162;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #646.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 31; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 6 BP; 0 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTCG 6


RESULT 7
ABN73675/c
```

```
ID   ABN73675 standard; cDNA; 6 BP.
XX
AC   ABN73675;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 21.
XX
KW   Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW   development; gene; ss.
XX
OS   Bos taurus.
XX
PN   WO200194550-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018576.
XX
PR   07-JUN-2000; 2000US-0209874P.
PR   06-JUN-2001; 2001US-00876143.
XX
PA   (INFI-) INFIGEN INC.
XX
PI   Eilertsen KJ,  Pfister-Genskow M,  Childs L;
XX
DR   WPI; 2002-351289/38.
XX
PT   An expressed sequence tag (EST), the expression of which, or its
PT   complementary sequence, in a cell identifies the cell as a
PT   developmentally competent or incompetent cell.
XX
PS   Example 16; Page 213; 584pp; English.
XX
CC   The present invention describes an expressed sequence tag (EST), where
CC   the EST is an isolated, enriched, or purified nucleic acid sequence
CC   representing all or part of a gene, the expression of which, or its
CC   complementary sequence, in a cell identifies the cell as a
CC   developmentally competent or incompetent cell. Molecules which induce
CC   developmental competence in a cell line are useful for inducing
CC   totipotence in one or more cells. Molecules which induce developmental
CC   incompetence in a cell line are useful for preventing a full term
CC   pregnancy in an animal and inhibiting totipotence. The molecules are also
CC   useful for treating a disease in an animal by inducing development of one
CC   or more cells of the animal into a specific cell type. The present
CC   sequence represents a bovine EST which is given in the exemplification of
CC   the present invention
XX
SQ   Sequence 6 BP; 4 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 8
ABS65900
ID   ABS65900 standard; DNA; 6 BP.
XX
AC   ABS65900;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Inhibitory oligonucleotide specific for hepatitis C virus #106.
XX
KW   Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW   non-B hepatitis; acute hepatitis; chronic hepatitis;
KW   hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KW   gene therapy; ss.
```

XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PF 02-JUL-1997; 97US-00887505.
XX
PR 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX
PA (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
DR WPI; 2002-537132/57.
XX
PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
PS Claim 1; Page 6; 74pp; English.
XX
CC The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic oligonucleotide used for inhibiting HCV
CC replication and expression of HCV
XX
SQ Sequence 6 BP; 1 A; 0 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 6; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTTG 4

RESULT 9
ABK30086/c
ID ABK30086 standard; DNA; 6 BP.
XX
AC ABK30086;
XX
DT 23-APR-2002 (first entry)
XX
DE Beta-lactamase promoter, wild type -35 to -30 region.
XX
KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW vanH promoter; androgen receptor promoter; AR promoter;
KW human epidermal growth factor receptor 2 promoter; her2 promoter;
KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
KW colon cancer; immunological disorder; prostate cancer; cytostatic;
KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW gene expression modulator; multiple sclerosis; MS;
KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW mutant; transgenic; ds.
XX
OS Escherichia coli.
XX
PN WO200194600-A2.
XX
PD 13-DEC-2001.
XX
PF 06-JUN-2001; 2001WO-US018343.
XX
PR 06-JUN-2000; 2000US-0209549P.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
PI Lim MY, Bruice TW;
XX
DR WPI; 2002-130595/17.
XX
PT New nucleic acid regulatory sequences, which are able to regulate
PT expression of a gene operably linked to a promoter, useful for regulating
PT the expression of transgenes and for treating e.g., cancer and
PT immunological diseases.
XX
PS Example 7; Page 57; 95pp; English.
XX
CC The invention describes an isolated nucleic acid regulatory sequence for
CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
CC (Bla) promoter. Transcription regulatory sequences may be used to
CC regulate expression of the endogenous, autologous or heterologous genes
CC operably linked to the promoter, and may be incorporated into
CC heterologous nucleic acid constructs for use in regulated expression of
CC transgenes. Regulated expression of cyclin D1 can be used in cancer
CC therapies, such as breast, colon or pancreatic cancers and familial
CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
CC may be used in the treatment of immunological disorders, such as
CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
CC arthritis. Regulated expression of genes under the control of the HBV
CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
CC hepatocellular carcinoma, and in the regulated expression of liver cell-
CC specific genes. Regulated expression of the vanH gene promoter can be
CC used in treatment of Enterococcus infection, while regulated expression
CC of the androgen receptor gene can be used in the treatment of prostate
CC cancer. This sequence represents a mutated promoter region used in the
CC invention to determine the regulatory regions involved in gene
CC expression, described in the method of the invention
XX
SQ Sequence 6 BP; 3 A; 1 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 6; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 6 TTTG 3

RESULT 10
ACD99934
ID ACD99934 standard; DNA; 6 BP.
XX

AC ACD99934;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #620.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 25; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 6 BP; 0 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 9; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 3 TTCG 6

RESULT 11
ACH50857/c
ID ACH50857 standard; DNA; 6 BP.
XX
AC ACH50857;
XX
DT 13-OCT-2003 (first entry)
XX
DE Hypothetical positively hybridised probe #3 extension probe #1.
XX
KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW biodiversity; genetic disorder.
XX
OS Synthetic.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Example 19; Page 36; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is a hypothetical probe used to illustrate a method of
CC detecting/determining mutations and polymorphisms
XX
SQ Sequence 6 BP; 4 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 9; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 12
ACH50858/c
ID ACH50858 standard; DNA; 6 BP.
XX
AC ACH50858;
XX
DT 13-OCT-2003 (first entry)
XX
DE Hypothetical positively hybridised probe #3 extension probe #2.
XX
KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW biodiversity; genetic disorder.
XX
OS Synthetic.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.

```
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Example 19; Page 36; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 3 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 13
ACH50860/c
ID   ACH50860 standard; DNA; 6 BP.
XX
AC   ACH50860;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Hypothetical positively hybridised probe #3 extension probe #4.
XX
KW   Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW   biodiversity; genetic disorder.
XX
OS   Synthetic.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Example 19; Page 36; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 3 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 14
ACH50845/c
ID   ACH50845 standard; DNA; 6 BP.
XX
AC   ACH50845;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Hypothetical negatively hybridised probe #1.
XX
KW   Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW   biodiversity; genetic disorder.
XX
OS   Synthetic.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
```

XX
PS Example 19; Page 36; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is a hypothetical probe used to illustrate a method of
CC detecting/determining mutations and polymorphisms
XX
SQ Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 9; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 15
ACH50859/c
ID ACH50859 standard; DNA; 6 BP.
XX
AC ACH50859;
XX
DT 13-OCT-2003 (first entry)
XX
DE Hypothetical positively hybridised probe #3 extension probe #3.
XX
KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW biodiversity; genetic disorder.
XX
OS Synthetic.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Example 19; Page 36; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is a hypothetical probe used to illustrate a method of
CC detecting/determining mutations and polymorphisms
XX
SQ Sequence 6 BP; 3 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 9; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 16
ACH50850/c
ID ACH50850 standard; DNA; 6 BP.
XX
AC ACH50850;
XX
DT 13-OCT-2003 (first entry)
XX
DE Hypothetical positively hybridised probe #2 extension probe #3.
XX
KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW biodiversity; genetic disorder.
XX
OS Synthetic.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Example 19; Page 36; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide

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CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 3 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 17
ACH50849/c
ID   ACH50849 standard; DNA; 6 BP.
XX
AC   ACH50849;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Hypothetical positively hybridised probe #2 extension probe #2.
XX
KW   Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW   biodiversity; genetic disorder.
XX
OS   Synthetic.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Example 19; Page 36; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 3 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 18
ACH50851/c
ID   ACH50851 standard; DNA; 6 BP.
XX
AC   ACH50851;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Hypothetical positively hybridised probe #2 extension probe #4.
XX
KW   Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW   biodiversity; genetic disorder.
XX
OS   Synthetic.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58..
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Example 19; Page 36; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 3 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 19
ACH50848/c
ID   ACH50848 standard; DNA; 6 BP.
XX
AC   ACH50848;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Hypothetical positively hybridised probe #2 extension probe #1.
XX
KW   Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW   biodiversity; genetic disorder.
XX
OS   Synthetic.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Example 19; Page 36; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 4 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 20
ACH50843/c
ID   ACH50843 standard; DNA; 6 BP.
XX
AC   ACH50843;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Hypothetical positively hybridised probe #1.
XX
KW   Probe; ss; sequencing by hybridisation; SBH; genome mapping;
KW   biodiversity; genetic disorder.
XX
OS   Synthetic.
XX
PN   US2003073623-A1.
XX
PD   17-APR-2003.
XX
PF   30-JUL-2001; 2001US-00918995.
XX
PR   30-JUL-2001; 2001US-00918995.
XX
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
XX
PI   Drmanac RT,  Labat I,  Stache-Crain B,  Dickson MC,  Jones LW;
XX
DR   WPI; 2003-615964/58.
XX
PT   New polynucleotide sequences obtained from various cDNA libraries, useful
PT   as hybridization probes, as oligomers for PCR, for chromosome and gene
PT   mapping, in the recombinant production of protein, or in generating
PT   antisense DNA or RNA.
XX
PS   Example 19; Page 36; 44pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising any one of
CC   38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC   determined by the technique of SBH (sequencing by hybridisation). Also
CC   included is a purified polypeptide comprising a sequence corresponding to
CC   a reading frame of the novel polynucleotide. The nucleic acid sequences
CC   are useful in diagnostics as expressed sequence tags (EST) for
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is a hypothetical probe used to illustrate a method of
CC   detecting/determining mutations and polymorphisms
XX
SQ   Sequence 6 BP; 3 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 6;
  Best Local Similarity  25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 3


RESULT 21
ADR33065/c
ID   ADR33065 standard; DNA; 6 BP.
XX
AC   ADR33065;
XX
```

DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #606.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 81; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 3 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 5 TTTG 2

RESULT 22
ADR33243/c
ID ADR33243 standard; DNA; 6 BP.
XX
AC ADR33243;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #784.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 84; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 4 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 1

RESULT 23
ADR33006/c

```
ID   ADR33006 standard; DNA; 6 BP.
XX
AC   ADR33006;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent target DNA #547.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 1; Page 80; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. This sequence
CC   corresponds to nucleic acid used in the method of the invention.
XX
SQ   Sequence 6 BP; 3 A; 1 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2
```

```
RESULT 24
ADR33007/c
ID   ADR33007 standard; DNA; 6 BP.
XX
AC   ADR33007;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent target DNA #548.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 1; Page 80; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. This sequence
CC   corresponds to nucleic acid used in the method of the invention.
XX
SQ   Sequence 6 BP; 3 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 3
```

RESULT 25
ADR32753
ID ADR32753 standard; DNA; 6 BP.
XX
AC ADR32753;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #294.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 76; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 2 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 3 TTCG 6

RESULT 26
ADR33260/c
ID ADR33260 standard; DNA; 6 BP.
XX
AC ADR33260;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #801.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 84; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 6;
Best Local Similarity 25.0%; Pred. No. 9.5e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 27
ADR32558
ID   ADR32558 standard; DNA; 6 BP.
XX
AC   ADR32558;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent target DNA #99.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 1; Page 73; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. This sequence
CC   corresponds to nucleic acid used in the method of the invention.
XX
SQ   Sequence 6 BP; 1 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 9.5e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 28
AAQ45285/c
ID   AAQ45285 standard; rRNA; 7 BP.
XX
AC   AAQ45285;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1994  (first entry)
XX
DE   Sequence of loop III in D10 epitope.
XX
KW   D10 epitope; g10 antibody; control RNA; loop sequence; ss.
XX
OS   Synthetic.
XX
PN   WO9406934-A1.
XX
PD   31-MAR-1994.
XX
PF   31-AUG-1993;   93WO-US008210.
XX
PR   11-SEP-1992;   92US-00944208.
PR   30-SEP-1992;   92US-00956693.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Keene JD,  Kenan DJ,  Tsai DE;
XX
DR   WPI; 1994-118482/14.
XX
PT   Generating nucleic acid epitopes cross-reactive with non-nucleic acid
PT   immunogens, pref. viruses and allergens - used to generate immune
PT   responses in humans and animals.
XX
PS   Example; Page 33; 56pp; English.
XX
CC   Anti-g10 antibody is specific for proteins contg. a g10 fusion peptide
CC   (see AAR51052). However, whereas the g10 peptide is a useful epitope tag
CC   for analysing complexes contg. protein, an RNA epitope tag would be
CC   equally useful for studying complexes contg. RNA. The anti-g10 serum was
CC   presented with a degenerate pool of RNA contg. 1,048,576 species
CC   representing all possible RNA species. The transcripts were
CC   immunoprecipitated with the anti-g10 serum. A single RNA species, D10,
CC   was obtd. RNAs tagged with the D10 RNA epitope were immunoprecipitated.
CC   For example, U1 RNA was tagged with the D10 epitope by replacing loop
CC   III, sequence AAQ45285, with the sequence in AAQ45286. (Updated on 25-MAR
CC   -2003 to correct PN field.)
XX
SQ   Sequence 7 BP; 3 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 2;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 29
AAT75839
ID   AAT75839 standard; rRNA; 7 BP.
XX
AC   AAT75839;
XX
```

DT 10-SEP-1997 (first entry)
XX
DE Corynebacterium pilosum 16S rRNA (from region 195-215).
XX
KW Ribosomal RNA; species specific; detection; reverse transcription;
KW primer; hybridisation probe; identification; ss.
XX
OS Corynebacterium pilosum.
XX
PN FR2733755-A1.
XX
PD 08-NOV-1996.
XX
PF 03-MAY-1995; 95FR-00005494.
XX
PR 03-MAY-1995; 95FR-00005494.
XX
PA (INMR) BIO MERIEUX.
XX
PI Mabilat C, Ruimy R;
XX
DR WPI; 1997-001738/01.
XX
PT Fragments of Corynebacterium 16S RNA - useful as probes and primers for
PT identifying Corynebacterium spp.
XX
PS Claim 2; Page 16; 60pp; French.
XX
CC Fragments covering 90 % of the sequence of 16S ribosomal RNA were
CC amplified from 28 strains of 25 different species of Corynebacterium by
CC PCR using primers specific for eubacteria. The amplification products
CC were sequenced and the sequences were aligned for comparison. It was
CC found that certain regions, i.e. those corresponding to nucleotides 72-
CC 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S
CC ribosomal RNA of C. diphtheriae, vary considerably between different
CC species. Probes and primers comprising at least 5 nucleotides from one of
CC these species-specific sequences, including the present sequence, or
CC their complements, are useful to distinguish between different
CC Corynebacterium species. DNA versions of the probes and primers are also
CC included
XX
SQ Sequence 7 BP; 0 A; 1 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 8.2e+08;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
||:|
Db 2 UUUG 5

RESULT 30
AAV58899
ID AAV58899 standard; DNA; 7 BP.
XX
AC AAV58899;
XX
DT 20-JAN-1999 (first entry)
XX
DE Leptospira nucleotide sequence.
XX
KW Infection; pathogenic Leptospira; protective immunity; therapy;
KW diagnosis; ss.
XX
OS Leptospira sp.
XX
PN WO9840099-A1.
XX
PD 17-SEP-1998.
XX
PF 06-MAR-1998; 98WO-AU000145.
XX
PR 07-MAR-1997; 97AU-00005494.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (PIGR-) PIG RES & DEV CORP.
XX
PI Chappel RJ;
XX
DR WPI; 1998-520791/44.
XX
PT New isolated pathogenic Leptospira bacterium - useful for, e.g developing
PT products for conferring protective immunity, and for prophylactic or
PT therapeutic treatment.
XX
PS Claim 15; Page 72; 94pp; English.
XX
CC This sequence represents a Leptospira DNA sequence isolated from the
CC pathogenic Leptospira (LS) bacterium of the invention. The bacterium
CC belongs to serogroup Hurstbridge or serovar hurstbridge or the species L.
CC fainei. The LS bacteria can be used for conferring protective immunity
CC against pathogenic LS bacteria in humans or animals. The bacteria can
CC also be used for prophylactic or therapeutic treatment of LS infections.
CC The DNAs and antibodies may also be used for detection and diagnosis of
CC past or present LS infection
XX
SQ Sequence 7 BP; 2 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTTG 4

RESULT 31
AAA27964
ID AAA27964 standard; DNA; 7 BP.
XX
AC AAA27964;
XX
DT 15-AUG-2000 (first entry)
XX
DE Box W1 weak elicitor-responsive cis-element nucleotide sequence.
XX
KW Box W1; elicitor-responsive cis-element; parsley; PR1 promoter; ss;
KW chimeric promoter; pathogen infection; transgenic plant; resistance;
KW herbicide; local response; genetic engineering; disease resistant crop.
XX
OS Petroselinum crispum.
XX
PN WO200029592-A2.
XX
PD 25-MAY-2000.
XX
PF 12-NOV-1999; 99WO-EP008710.
XX
PR 12-NOV-1998; 98EP-00121160.
PR 27-AUG-1999; 99EP-00116981.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG.
XX
PI Kirsch C, Logemann E, Hahlbrock K, Rushton P, Somssich I;
XX
DR WPI; 2000-387804/33.
XX
PT Chimeric promoters mediating gene expression in plants upon pathogen
PT infection, useful for transgenic plant production comprises at least one
PT cis-acting element to direct elicitor-specific expression.
XX
PS Claim 2; Page 32; 73pp; English.
XX
CC This sequence represents Box W1, a weak elicitor-responsive cis-element

CC from the Parsley PR1 promoter. The present invention relates to chimeric
CC promoters capable of mediating local gene expression in plants upon
CC pathogen infection. The chimeric promoters comprise at least one cis-
CC element (see AAA27964-A27979) capable of directing elicitor-specific
CC expression, and a minimal promoter. The chimeric promoters are useful for
CC producing a transgenic plant which has attained resistance or improved
CC resistance against a pathogen. The cis-acting element, chimeric promoter,
CC recombinant gene encoding the chimeric promoter, vector comprising the
CC chimeric promoter and a compound capable of activating the chimeric
CC promoter are useful for producing pathogen resistant plants, and for
CC identifying and/or producing compounds capable of conferring induced
CC resistance to a pathogen in a plant. A compound which specifically
CC activates or inhibits genes activated in a plant when attacked by a
CC pathogen is also useful as a plant protective agent or a herbicide. The
CC chimeric promoter provides rapid and local response to pathogen attack
CC but shows negligible activity in uninfected parts of the plants and
CC therefore is most suitable for the engineering of disease resistant crops
XX
SQ Sequence 7 BP; 1 A; 2 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTTG 4

RESULT 32
AAZ48430
ID AAZ48430 standard; DNA; 7 BP.
XX
AC AAZ48430;
XX
DT 27-MAR-2000 (first entry)
XX
DE Bacteria specific nucleic acid sequence.
XX
KW Microorganism; virus; polymerase chain reaction; food; cosmetic;
KW clinical diagnostic; molecular beacon; ss.
XX
OS Synthetic.
XX
PN WO9963112-A2.
XX
PD 09-DEC-1999.
XX
PF 18-MAY-1999; 99WO-US010940.
XX
PR 18-MAY-1998; 98US-0086025P.
PR 17-MAY-1999; 99US-00086025.
XX
PA (HUNT-) HUNT WESSON INC.
XX
PI Romick TL, Fraser MS;
XX
DR WPI; 2000-086985/07.
XX
PT Detection of microorganisms and viruses, for use in the food and cosmetic
PT industries and for clinical diagnostics.
XX
PS Claim 36; Page 38; 63pp; English.
XX
CC The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
CC comprising 5'-GCTAAGGTCCCAAAGT-3', and a second primer comprising 5'-
CC AGAACGCTCTCCTACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
CC to replicate and attain 0.25-10000mug nucleotide product/mul mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTCTAAGCCACC-3' to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC probe; and (4) determining whether or not bacteria are present in the
CC sample by detecting the conformational change of the probe, a
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,
CC including bacteria, yeast, molds and protista. They can be used in the
CC food and cosmetic industry and in clinical diagnostics. Using the method
CC it is not necessary to remove non-hybridized probe from the system
XX
SQ Sequence 7 BP; 1 A; 2 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 3; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTCG 7

RESULT 33
AAZ48459/c
ID AAZ48459 standard; DNA; 7 BP.
XX
AC AAZ48459;
XX
DT 27-MAR-2000 (first entry)
XX
DE Nucleic acid fragment used in detection of microorganisms.
XX
KW Microorganism; virus; polymerase chain reaction; food; cosmetic;
KW clinical diagnostic; molecular beacon; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO9963112-A2.
XX
PD 09-DEC-1999.
XX
PF 18-MAY-1999; 99WO-US010940.
XX
PR 18-MAY-1998; 98US-0086025P.
PR 17-MAY-1999; 99US-00086025.
XX
PA (HUNT-) HUNT WESSON INC.
XX
PI Romick TL, Fraser MS;
XX
DR WPI; 2000-086985/07.
XX
PT Detection of microorganisms and viruses, for use in the food and cosmetic
PT industries and for clinical diagnostics.
XX
PS Claim 36; Page 38; 63pp; English.
XX
CC The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
CC comprising 5'-GCTAAGGTCCCAAAGT-3', and a second primer comprising 5'-
CC AGAACGCTCTCCTACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
CC to replicate and attain 0.25-10000mug nucleotide product/mul mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTCTAAGCCACC-3' to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC probe; and (4) determining whether or not bacteria are present in the
CC sample by detecting the conformational change of the probe, a
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,

```
CC   including bacteria, yeast, molds and protista. They can be used in the
CC   food and cosmetic industry and in clinical diagnostics. Using the method
CC   it is not necessary to remove non-hybridized probe from the system
XX
SQ   Sequence 7 BP; 3 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 3;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 1


RESULT 34
AAD32130
ID   AAD32130 standard; DNA; 7 BP.
XX
AC   AAD32130;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Linker/Adapter BE1R to construct representative expression library.
XX
KW   Subtractive hybridisation; nucleic acid isolation technique;
KW   visual identification; ss.
XX
OS   Unidentified.
XX
PN   WO200210458-A2.
XX
PD   07-FEB-2002.
XX
PF   02-AUG-2001; 2001WO-US024480.
XX
PR   02-AUG-2000; 2000US-00631349.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer LG,  Leary TP,  Muerhoff AS,  Desai SM,  Mushahwar IK;
XX
DR   WPI; 2002-269020/31.
XX
PT   Improved method for performing subtractive hybridization useful in
PT   nucleic acid isolation techniques, by employing Selective Primed Adaptive
PT   Driver-RDA, which utilizes a tester sample and a driver sample.
XX
PS   Example 7; Page 33; 67pp; English.
XX
CC   The invention relates to an improved method for performing subtractive
CC   hybridisation. The method involves using a tester sample and a driver
CC   sample to determine the presence of a nucleic acid sequence difference in
CC   the tester sample. The method is useful for performing subtractive
CC   hybridisation particularly for improving nucleic acid isolation
CC   techniques. The method may also be used for the visual identification of
CC   unique tester sequences. The present sequence is a linker/adapter used
CC   for constructing a representative expression library used in the
CC   exemplification of the invention
XX
SQ   Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 7


RESULT 35
ABK88715/c
ID   ABK88715 standard; DNA; 7 BP.
XX
AC   ABK88715;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Human CD95 gene transcription silencer heptamer sequence #2.
XX
KW   Human; apoptotic cell death; proteinaceous transcription factor;
KW   regulation of gene transcription; apoptosis; p53; CD95; TRA;
KW   transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
KW   tumour cell; embryonic cell; nervous system; intracellular pathogen;
KW   DNA-damaging agent; retroviral infection; neurodegenerative disorder;
KW   immune system dysfunction; anti-tumour; cytostatic; hCD95;
KW   transcription silencer region; ds.
XX
OS   Homo sapiens.
XX
PN   WO200244363-A1.
XX
PD   06-JUN-2002.
XX
PF   28-NOV-2001; 2001WO-NZ000287.
XX
PR   28-NOV-2000; 2000US-00724809.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Lasham A,  Watson JD;
XX
DR   WPI; 2002-557540/59.
XX
PT   Modulating p53-mediated apoptotic cell death in a population of cells, by
PT   modulating the amount of a transcriptional regulator of apoptosis
PT   available to bind to a target polynucleotide in the cells.
XX
PS   Example 1; Page 55; 62pp; English.
XX
CC   The present invention relates to methods for modulating apoptotic cell
CC   death using proteinaceous transcription factors that regulate the
CC   transcription of genes encoding proteins involved in apoptosis (e.g. CD95
CC   and p53). The methods involve modulating the amount of a transcriptional
CC   regulator of apoptosis (TRA) available to bind to a target polynucleotide
CC   in the cells, where TRA is a member of the Y-box nucleic acid binding
CC   family of polypeptides (e.g. YB-1). The methods of the invention are
CC   useful for modulating apoptotic cell death in a population of cells,
CC   where the cells are selected from tumour cells, cells of the immune
CC   system, embryonic cells, cells of the nervous system, or cells infected
CC   with intracellular pathogens. The methods are also useful for increasing
CC   the sensitivity of tumour cells to a DNA-damaging agent, and for
CC   increasing sensitivity to apoptosis in a population of cells harbouring
CC   intracellular pathogens. The methods are useful for screening an
CC   apoptosis modulatory agent that modulates the binding of TRA. The methods
CC   for regulating apoptosis can be used therapeutically and prophylactically
CC   for various disorders such as cancer, viral and retroviral infections,
CC   neurodegenerative disorders, and immune system dysfunction. The present
CC   sequence represents a transcription silencer heptamer motif present in
CC   the human CD95 (hCD95) gene
XX
SQ   Sequence 7 BP; 4 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          7 TTTG 4


RESULT 36
ABK88705
ID   ABK88705 standard; DNA; 7 BP.
```

XX
AC ABK88705;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human CD95 gene transcription silencer heptamer sequence #1.
XX
KW Human; apoptotic cell death; proteinaceous transcription factor;
KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
KW immune system dysfunction; anti-tumour; cytostatic; hCD95;
KW transcription silencer region; ds.
XX
OS Homo sapiens.
XX
PN WO200244363-A1.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-NZ000287.
XX
PR 28-NOV-2000; 2000US-00724809.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Lasham A, Watson JD;
XX
DR WPI; 2002-557540/59.
XX
PT Modulating p53-mediated apoptotic cell death in a population of cells, by
PT modulating the amount of a transcriptional regulator of apoptosis
PT available to bind to a target polynucleotide in the cells.
XX
PS Example 1; Page 54; 62pp; English.
XX
CC The present invention relates to methods for modulating apoptotic cell
CC death using proteinaceous transcription factors that regulate the
CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
CC and p53). The methods involve modulating the amount of a transcriptional
CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
CC in the cells, where TRA is a member of the Y-box nucleic acid binding
CC family of polypeptides (e.g. YB-1). The methods of the invention are
CC useful for modulating apoptotic cell death in a population of cells,
CC where the cells are selected from tumour cells, cells of the immune
CC system, embryonic cells, cells of the nervous system, or cells infected
CC with intracellular pathogens. The methods are also useful for increasing
CC the sensitivity of tumour cells to a DNA-damaging agent, and for
CC increasing sensitivity to apoptosis in a population of cells harbouring
CC intracellular pathogens. The methods are useful for screening an
CC apoptosis modulatory agent that modulates the binding of TRA. The methods
CC for regulating apoptosis can be used therapeutically and prophylactically
CC for various disorders such as cancer, viral and retroviral infections,
CC neurodegenerative disorders, and immune system dysfunction. The present
CC sequence represents a transcription silencer heptamer motif present in
CC the human CD95 (hCD95) gene
XX
SQ Sequence 7 BP; 1 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 6; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTTG 4

RESULT 37
ACD56778
ID ACD56778 standard; RNA; 7 BP.
XX
AC ACD56778;
XX
DT 24-SEP-2003 (first entry)
XX
DE Synthetic RNA sequence #23 used in HBV RT modulation experiment.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; ss.
XX
OS Synthetic.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Example 13; Page 230; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a synthetic nucleic acid
CC molecule used in HBV RT modulation experiments
XX
SQ Sequence 7 BP; 2 A; 1 C; 2 G; 0 T; 2 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 8; Length 7;
Best Local Similarity 75.0%; Pred. No. 8.2e+08;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 UUYG 4
              ||:|
Db          4 UUCG 7


RESULT 38
ACD56769
ID   ACD56769 standard; RNA; 7 BP.
XX
AC   ACD56769;
XX
DT   24-SEP-2003  (first entry)
XX
DE   Synthetic RNA sequence #14 used in HBV RT modulation experiment.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; ss.
XX
OS   Synthetic.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Example 13; Page 230; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a synthetic nucleic acid
CC   molecule used in HBV RT modulation experiments
XX
SQ   Sequence 7 BP; 2 A; 1 C; 2 G; 0 T; 2 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 8;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 8.2e+08;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              ||:|
Db          4 UUCG 7


RESULT 39
ADA36984
ID   ADA36984 standard; RNA; 7 BP.
XX
AC   ADA36984;
XX
DT   20-NOV-2003  (first entry)
XX
DE   RNA oligonucleotide component of uGL3.7RNA SEQ ID NO:4.
XX
KW   single-stranded polynucleotide; cytostatic; virucide;
KW   antiarteriosclerotic; anti-HIV; RNA inhibition; gene therapy;
KW   antisense therapy; RNase inhibitor; genetic disease; infection; cancer;
KW   AIDS; arteriosclerosis; ss.
XX
OS   Synthetic.
XX
PN   WO2003070932-A1.
XX
PD   28-AUG-2003.
XX
PF   21-FEB-2003; 2003WO-JP001913.
XX
PR   22-FEB-2002; 2002JP-00046889.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
PI   Suzuki M,  Momota H,  Watanabe T;
XX
DR   WPI; 2003-646626/61.
XX
PT   Single-stranded polynucleotide for target gene, useful in developing
PT   drugs for treatment of genetic diseases and infections, e.g. cancer, AIDS
PT   and arteriosclerosis.
XX
PS   Claim 11; Page 63; 71pp; Japanese.
XX
CC   The present invention describes an isolated or purified single-stranded
CC   polynucleotide sequence for a target gene comprises components (I)-(III):
CC   (a) (I) is a polynucleotide sequence complementary to component (III);
CC   (b) (II) is a nucleotide sequence of 0-50 kilobases long (0 base = bond)
CC   or non-nucleotide sequence; and (c) (III) is complementary to any of the
CC   above, has RNA inhibitory activity and has 15-30 consecutive
CC   complementary strands to the target gene. The single-stranded
CC   polynucleotide sequence has cytostatic, virucide, antiarteriosclerotic
CC   and anti-HIV, and can be used for RNA inhibition, gene therapy, antisense
CC   therapy and as an RNase inhibitor. The polynucleotide is useful in
CC   developing drugs for treatment of genetic diseases and infections, e.g.
CC   cancer, AIDS and arteriosclerosis. The present sequence represents an RNA
CC   oligonucleotide used in the exemplification of the present invention.
XX
SQ   Sequence 7 BP; 0 A; 2 C; 1 G; 0 T; 4 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 8.2e+08;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 UUYG 4
              ||:|
Db          1 UUUG 4


RESULT 40
ADH76936/c
ID   ADH76936 standard; DNA; 7 BP.
XX
AC   ADH76936;
XX
DT   22-APR-2004  (first entry)
XX
DE   DNA motif recognised by all SOX members.
XX
KW   SOX18; ds; cell differentiation; vasculogenesis; angiogenesis;
KW   hair follicle development; MEF2C; atherosclerosis; cancer; restenosis;
KW   pulmonary disease; tissue injury; hair loss; tumourigenesis;
KW   subgroup F SOX; HMG domain; trans-activation domain;
KW   conserved C terminal domain; arterial wall; vascular smooth muscle;
KW   blood supply; cardiovascular disorder; ischaemic heart injury;
KW   neo-vascularisation; atherosclerotic plaque;
KW   double balloon intravascular catheter; gene transfer;
KW   fibroblast growth factor-1; FGF-1; platelet derived growth factor; PDGF;
KW   femoral artery; intimal hyperplasia; matrix deposition; gene therapy;
KW   cytostatic; antiarteriosclerotic; vasotropic.
XX
OS   Synthetic.
XX
PN   US2002142415-A1.
XX
PD   03-OCT-2002.
XX
PF   23-MAR-2001; 2001US-00814777.
XX
PR   24-MAR-2000; 2000AU-00006457.
XX
PA   (KOOP/) KOOPMAN P A.
PA   (MUSC/) MUSCAT G E O.
XX
PI   Koopman PA,  Muscat GEO;
XX
DR   WPI; 2003-155943/15.
XX
PT   Novel SOX18 polypeptide useful for modulating cell differentiation,
PT   vasculogenesis, angiogenesis, hair follicle development, cell
PT   proliferation and tumorigenesis.
XX
PS   Example 8; SEQ ID NO 58; 148pp; English.
XX
CC   The invention discloses an isolated SOX18 polypeptides, given in the
CC   specification, and biologically active fragments having at least 6 amino
CC   acids in length, or variants having at least 85% sequence identity. Also
CC   claimed are isolated polynucleotides encoding the polypeptides; isolated
CC   polynucleotides encoding polypeptides which modulates an activity
CC   selected from cell differentiation, vasculogenesis, angiogenesis, hair
CC   follicle development; detecting a specific polypeptide or polynucleotide
CC   sequence; detecting a SOX18 polypeptide, by contacting a test polypeptide
CC   with a MEF2C polypeptide in a biological sample; an antigen-binding
CC   molecule that is specifically immuno-interactive; detecting the activity
CC   selected from cell differentiation, vasculogenesis, angiogenesis and hair
CC   follicle development; a composition for treatment and/or prophylaxis of
CC   at least one condition selected from atherosclerosis, cancer, restenosis,
CC   pulmonary disease, tissue injury and hair loss, comprising a SOX18
CC   polypeptide and an agent that enhances the level and/or functional
CC   activity of the polypeptide, together with a carrier; a composition for
CC   treatment and/or prophylaxis of tumourigenesis, comprising an agent that
CC   reduces the level and/or functional activity of at least one subgroup F
CC   SOX polypeptide, together with a carrier and a composition comprising one
CC   or more agents that enhances the level and/or functional activity of at
CC   least two subgroup F SOX polypeptides. The biologically active fragment
CC   is at least 8 amino acids in length and comprises a SOX18 HMG domain,
CC   SOX18 trans-activation domain, SOX18 conserved C terminal domain, or a
CC   portion of the domain having at least 6 amino acids in length. Delivery
CC   of recombinant Sox18 into arterial walls had use in the stimulation of
CC   vascular smooth muscle cells to improve blood supply and flow in a
CC   several cardiovascular disorders including ischaemic heart injury and the
CC   neo-vascularisation of atherosclerotic plaques. This was achieved using a
CC   similar double balloon intravascular catheter mediated gene transfer
CC   approach of fibroblast growth factor (FGF)-1 and platelet derived growth
CC   factor (PDGF) into the femoral arteries resulted in induced intimal
CC   hyperplasia, angiogenesis and matrix deposition. The polynucleotides may
CC   be used in gene therapy. The sequence presented is a DNA motif recognised
CC   by all SOX members.
XX
SQ   Sequence 7 BP; 5 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 3.6;  DB 10;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 3


RESULT 41
ADR36886
ID   ADR36886 standard; DNA; 7 BP.
XX
AC   ADR36886;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #3306.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
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CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 7 BP; 2 A; 0 C; 1 G; 3 T; 0 U; 1 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 7

RESULT 42
ADR33128/c
ID ADR33128 standard; DNA; 7 BP.
XX
AC ADR33128;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #669.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 82; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 7 BP; 3 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 6 TTTG 3

RESULT 43
ADR36888
ID ADR36888 standard; DNA; 7 BP.
XX
AC ADR36888;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #3308.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism

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CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 7 BP; 2 A; 0 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 44
ADR36887
ID   ADR36887 standard; DNA; 7 BP.
XX
AC   ADR36887;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #3307.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 7 BP; 2 A; 0 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             90.0%;  Score 3.6;  DB 13;  Length 7;
  Best Local Similarity   25.0%;  Pred. No. 8.2e+08;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 45
ADR36885
ID   ADR36885 standard; DNA; 7 BP.
XX
AC   ADR36885;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #3305.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
```

CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 7 BP; 2 A; 0 C; 1 G; 3 T; 0 U; 1 Other;

Query Match 90.0%; Score 3.6; DB 13; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.2e+08;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 4 TTTG 7

Search completed: April 4, 2005, 11:53:12
Job time : 287 secs

OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:03:06 ; Search time 2036 Seconds
(without alignments)
74.782 Million cell updates/sec

Title: US-10-748-475-1
Perfect score: 4
Sequence: 1 uuyg 4

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3.6	90.0	5	9	CL667999	CL667999 PRI0156c_
	2	3.6	90.0	5	9	CL685291	CL685291 PRI0140d_
c	3	3.6	90.0	6	6	CA850767	CA850767 D06C11_C1
c	4	3.6	90.0	6	6	CA851592	CA851592 D15D09_G2
c	5	3.6	90.0	6	7	CF309881	CF309881 ABF--04-E
	6	3.6	90.0	7	1	AL042652	AL042652 DKFZp434N
c	7	3.6	90.0	7	7	CF324531	CF324531 HDN--06-M
	8	3.6	90.0	7	9	CL423561	CL423561 01S0557-0
	9	3.6	90.0	7	9	CL682672	CL682672 PRI0134c_
c	10	3.6	90.0	8	6	CD746149	CD746149 S10_E09_S
	11	3.6	90.0	8	7	CF312042	CF312042 ABF--07-J
	12	3.6	90.0	8	7	CF320404	CF320404 HD--11-E1
	13	3.6	90.0	9	6	CA850970	CA850970 D08G04_N1
c	14	3.6	90.0	9	6	CA851674	CA851674 D16C10_F2
c	15	3.6	90.0	9	9	CNS06E5N	AL394689 T3 end of
	16	3.6	90.0	9	9	CL314040	CL314040 mth2-130O
	17	3.6	90.0	10	9	AJ587649	AJ587649 Arabidops
	18	3.6	90.0	10	9	AJ587650	AJ587650 Arabidops
c	19	3.6	90.0	10	9	AJ593578	AJ593578 Arabidops
c	20	3.6	90.0	10	9	AJ594077	AJ594077 Arabidops
c	21	3.6	90.0	10	9	AJ594650	AJ594650 Arabidops
c	22	3.6	90.0	10	9	AJ599592	AJ599592 Arabidops
	23	3.6	90.0	10	9	AJ599908	AJ599908 Arabidops
c	24	3.6	90.0	10	9	AJ600523	AJ600523 Arabidops
	25	3.6	90.0	10	9	CL435887	CL435887 PST1710-2
	26	3.6	90.0	10	9	CL436026	CL436026 PST2176-N
c	27	3.6	90.0	10	9	CL436141	CL436141 PST2390-N
	28	3.6	90.0	10	9	CL436159	CL436159 PST2429-N
c	29	3.6	90.0	10	9	CL436183	CL436183 PST2465-N
	30	3.6	90.0	10	9	CL436207	CL436207 PST2511-N
	31	3.6	90.0	10	9	CL436277	CL436277 PST2644-N
	32	3.6	90.0	10	9	CL436725	CL436725 PST3688-N
c	33	3.6	90.0	10	9	CL437147	CL437147 PST4582-N
	34	3.6	90.0	10	9	CL437213	CL437213 PST4731-N
c	35	3.6	90.0	10	9	CL437237	CL437237 PST4801-N
c	36	3.6	90.0	10	9	CL437245	CL437245 PST4835-N
	37	3.6	90.0	10	9	CL437288	CL437288 PST4926-N
c	38	3.6	90.0	10	9	CL437389	CL437389 PST5280-N
	39	3.6	90.0	10	9	CL437824	CL437824 PST6362-N
c	40	3.6	90.0	10	9	CL437844	CL437844 PST6396-N
c	41	3.6	90.0	10	9	CL437917	CL437917 PST6521-N
c	42	3.6	90.0	10	9	CL437998	CL437998 PST6636-N
c	43	3.6	90.0	10	9	CL437999	CL437999 PST6637-N
	44	3.6	90.0	10	9	CL438166	CL438166 PST6939-N
	45	3.6	90.0	10	9	CL438191	CL438191 PST6982-N
	46	3.6	90.0	10	9	CL438272	CL438272 PST7181-N
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	48	3.6	90.0	10	9	CL438381	CL438381 PST7382-N
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	52	3.6	90.0	10	9	CL438642	CL438642 PST7937-N
c	53	3.6	90.0	10	9	CL438865	CL438865 PST8297-N
c	54	3.6	90.0	10	9	CL439403	CL439403 PST9180-N
c	55	3.6	90.0	10	9	CL439553	CL439553 PST9493-N
	56	3.6	90.0	10	9	CL439582	CL439582 PST9547-N
	57	3.6	90.0	10	9	CL679692	CL679692 PRI0126d_
	58	3.6	90.0	11	1	AL042478	AL042478 DKFZp434F
	59	3.6	90.0	11	1	AL042494	AL042494 DKFZp434G
	60	3.6	90.0	11	1	AL042526	AL042526 DKFZp434H
	61	3.6	90.0	11	4	BG927896	BG927896 HNC45-1-D
c	62	3.6	90.0	11	4	BM396042	BM396042 5009-0-15
c	63	3.6	90.0	11	5	BQ585171	BQ585171 S014222-0
	64	3.6	90.0	11	5	BQ587100	BQ587100 E012350-0
	65	3.6	90.0	11	5	BQ590709	BQ590709 E012597-0
c	66	3.6	90.0	11	7	CF306385	CF306385 HDA1--03-
c	67	3.6	90.0	11	7	CF542741	CF542741 S014678-0
	68	3.6	90.0	11	7	CF920900	CF920900 gmrhRww3-
	69	3.6	90.0	11	8	AQ445580	AQ445580 GSSTc0040
c	70	3.6	90.0	11	9	AJ587507	AJ587507 Arabidops
c	71	3.6	90.0	11	9	AJ587786	AJ587786 Arabidops
	72	3.6	90.0	11	9	AJ588245	AJ588245 Arabidops
c	73	3.6	90.0	11	9	AJ594614	AJ594614 Arabidops
	74	3.6	90.0	11	9	AJ598610	AJ598610 Arabidops
c	75	3.6	90.0	11	9	CL662987	CL662987 PRI0142d_
	76	3.6	90.0	12	1	AL042554	AL042554 DKFZp434I
c	77	3.6	90.0	12	5	BQ584779	BQ584779 E011673-0
c	78	3.6	90.0	12	5	BQ587870	BQ587870 S013708-0
	79	3.6	90.0	12	5	BQ589761	BQ589761 E012680-0
	80	3.6	90.0	12	5	BQ591624	BQ591624 E012618-0
c	81	3.6	90.0	12	5	BQ594595	BQ594595 E012444-0
c	82	3.6	90.0	12	5	BQ750930	BQ750930 EST631493
c	83	3.6	90.0	12	7	CF280439	CF280439 14ETL--07
c	84	3.6	90.0	12	7	CF307504	CF307504 HDA1--06-
	85	3.6	90.0	12	7	CF311119	CF311119 ABF--06-D
	86	3.6	90.0	12	8	AQ050979	AQ050979 nbxb0004d
c	87	3.6	90.0	12	8	BH169696	BH169696 SALK_0017
c	88	3.6	90.0	12	9	AJ587358	AJ587358 Arabidops
c	89	3.6	90.0	12	9	AJ593515	AJ593515 Arabidops
	90	3.6	90.0	12	9	AJ597080	AJ597080 Arabidops
	91	3.6	90.0	12	9	AJ597414	AJ597414 Arabidops
c	92	3.6	90.0	12	9	AJ600088	AJ600088 Arabidops
	93	3.6	90.0	12	9	AJ600541	AJ600541 Arabidops
c	94	3.6	90.0	12	9	CG677120	CG677120 tmf0875 t
	95	3.6	90.0	12	9	CL685356	CL685356 PRI0141a_
c	96	3.6	90.0	13	1	AI744941	AI744941 tr17e03.x
c	97	3.6	90.0	13	1	AJ647701	AJ647701 AJ647701

c 98	3.6	90.0	13	1	AJ648972	AJ648972 AJ648972
c 99	3.6	90.0	13	1	AJ681534	AJ681534 AJ681534
100	3.6	90.0	13	4	BM395395	BM395395 50072-2-8

ALIGNMENTS

RESULT 1
CL667999
LOCUS CL667999 5 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0156c_D12 - PRI0156c.B21 (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL667999
VERSION CL667999.1 GI:50162794
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 5)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

Query Match 90.0%; Score 3.6; DB 9; Length 5;
Best Local Similarity 25.0%; Pred. No. 7.6e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 2 TTTG 5

RESULT 2
CL685291
LOCUS CL685291 5 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0140d_C11_2 - PRI0140d.BR (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL685291
VERSION CL685291.1 GI:50193442
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 5)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

Query Match 90.0%; Score 3.6; DB 9; Length 5;
Best Local Similarity 25.0%; Pred. No. 7.6e+09;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 1 TTCG 4

RESULT 3
CA850767/c
LOCUS CA850767 6 bp mRNA linear EST 01-AUG-2003
DEFINITION D06C11_C11_05.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D06C11 5', mRNA sequence.
ACCESSION CA850767
VERSION CA850767.1 GI:33387560
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 6)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES Location/Qualifiers
source 1. .6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06C11"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
ORIGIN

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  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 6.3e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 4
CA851592/c
LOCUS       CA851592                  6 bp    mRNA    linear   EST 01-AUG-2003
DEFINITION  D15D09_G21_07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
            cDNA clone D15D09 5', mRNA sequence.
ACCESSION   CA851592
VERSION     CA851592.1  GI:33388385
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Alkharouf,N.W., Khan,R. and Matthews,B.F.
  TITLE     Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharon@ba.ars.usda.gov.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Peking"
                     /db_xref="taxon:3847"
                     /clone="D15D09"
                     /tissue_type="Roots"
                     /dev_stage="Seedlings"
                     /clone_lib="cDNA Peking library 2, 4 day SCN3"
                     /note="Vector: pBluescript SK-; cDNA clones from mRNA
                     extracted from Peking roots 2 and 4 days past invasion."
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 6.3e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 5
CF309881/c
LOCUS       CF309881                  6 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-E05.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--04-E05, mRNA sequence.
ACCESSION   CF309881
VERSION     CF309881.1  GI:33681642
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--04-E05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 7;  Length 6;
  Best Local Similarity   25.0%;  Pred. No. 6.3e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 6
AL042652
LOCUS       AL042652                  7 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  DKFZp434N1921_r1 434 (synonym: htes3) Homo sapiens cDNA clone
            DKFZp434N1921, mRNA sequence.
ACCESSION   AL042652
VERSION     AL042652.1  GI:49682449
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Blum, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp434N1921"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="434 (synonym: htes3)"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
```

```
  Query Match            90.0%;  Score 3.6;  DB 1;  Length 7;
  Best Local Similarity  25.0%;  Pred. No. 5.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 7
CF324531/c
LOCUS       CF324531                  7 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  HDN--06-M14.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
            clone HDN--06-M14, mRNA sequence.
ACCESSION   CF324531
VERSION     CF324531.1  GI:33797337
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HDN--06-M14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli SOLR"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
                     phage cDNA library II (HDN)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
                     5' end with EcoRI and 3' end with XhoI site. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 7;  Length 7;
  Best Local Similarity  25.0%;  Pred. No. 5.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          7 TTTG 4


RESULT 8
CL423561
LOCUS       CL423561                  7 bp    DNA     linear   GSS 16-MAR-2004
DEFINITION  01S0557-03B1-E05 UniformMu MuTAIL Library Zea mays genomic clone
            01S0557-03B1-E05, genomic survey sequence.
ACCESSION   CL423561
VERSION     CL423561.1  GI:45501605
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
  TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drm@ufl.edu
            Sequence Sequence flanking probable Mu insertion site in UniformMu
            line: 01S0557-03, Primer set: B
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="W22 (ACR, bz1-m9)"
                     /cultivar="UniformMu"
                     /db_xref="taxon:4577"
                     /clone="01S0557-03B1-E05"
                     /clone_lib="UniformMu MuTAIL Library"
                     /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                     insertions in Mu inactive lines were extracted from the
                     UniformMu maize population by the thermo assymmetric
                     interlaced PCR (TAIL) protocol using primers specific for
                     the Mu terminal inverted repeat and a set of 16 arbitrary
                     primers. Amplicons were size enriched using Sepharose 400
                     spin columns and cloned into the TOPO PCR4 vector."
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 7;
  Best Local Similarity  25.0%;  Pred. No. 5.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 7


RESULT 9
CL682672
LOCUS       CL682672                  7 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0134c_G06_2 - PRI0134c.BR (7) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL682672
VERSION     CL682672.1  GI:50190090
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
```

```
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 9;  Length 7;
  Best Local Similarity  25.0%;  Pred. No. 5.4e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTTG 4


RESULT 10
CD746149/c
LOCUS       CD746149                 8 bp    mRNA    linear   EST 25-JUN-2004
DEFINITION  S10_E09_S10_068.ab1 Sugar-fed (S) An.gam. 30 hr Abdomen Library
            Anopheles gambiae cDNA 5', mRNA sequence.
ACCESSION   CD746149
VERSION     CD746149.1  GI:49250116
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Dana,A.N., Lobo,N.F., Hillenmeyer,M.E. and Collins,F.H.
  TITLE     Hematophagy-associated gene expression patterns in adult female
            Anopheles gambiae mosquitoes
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Dana A.N.
            Frank H. Collins Laboratory
            University of Notre Dame
            Center for Tropical Disease Research and Training, Dept. of Biol.
            Sci., Notre Dame, IN 46556, USA
            Tel: 574 - 631 - 3241
            Fax: 574 - 631 - 3996
            Email: adana@nd.edu
            PCR PRimers
            FORWARD: ctcgggaagcgcgccattgtgttgg
            BACKWARD: atacgactcactatagggcgaattggc
            Seq primer: ctcgggaagcgcgccattgtgttgg.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="4Arr"
                     /db_xref="taxon:7165"
                     /sex="female"
                     /tissue_type="Abdomens"
                     /dev_stage="Female adult 5-7 days post eclosion"
                     /lab_host="E. coli XLI-Blue"
                     /clone_lib="Sugar-fed (S) An.gam. 30 hr Abdomen Library"
                     /note="Vector: lambdaTriplEx2 (Clontech); Site_1: Sfi IA;
                     Site_2: Sfi IB; Sugar-fed adult female An. gambiae
                     mosquitoes were flash frozen after a 30 hour incubation of
                     adult mosquitoes at 19 degrees Celsius. Total RNA
                     extracted from abdomens separated from remaining carcass.
                     CDNA inserts >500 bp cloned directionally into lTriplEx2;
                     Sfi IA site is 5'. Non-normalized and Non-amplified
                     phagemid library. Single pass sequencing reactions from 5'
                     end."
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 6;  Length 8;
  Best Local Similarity  25.0%;  Pred. No. 4.8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          8 TTTG 5


RESULT 11
CF312042
LOCUS       CF312042                 8 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-J07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--07-J07, mRNA sequence.
ACCESSION   CF312042
VERSION     CF312042.1  GI:33683803
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--07-J07"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
ORIGIN

  Query Match           90.0%;  Score 3.6;  DB 7;  Length 8;
  Best Local Similarity  25.0%;  Pred. No. 4.8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTCG 5


RESULT 12
CF320404
LOCUS       CF320404                 8 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-E15.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-E15, mRNA sequence.
ACCESSION   CF320404
VERSION     CF320404.1  GI:33692165
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
```

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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--11-E15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 7;  Length 8;
  Best Local Similarity   25.0%;  Pred. No. 4.8e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 13
CA850970
LOCUS       CA850970                  9 bp    mRNA    linear   EST 01-AUG-2003
DEFINITION  D08G04_N16_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
            cDNA clone D08G04 5', mRNA sequence.
ACCESSION   CA850970
VERSION     CA850970.1  GI:33387763
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Alkharouf,N.W., Khan,R. and Matthews,B.F.
  TITLE     Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharon@ba.ars.usda.gov.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Peking"
                     /db_xref="taxon:3847"
                     /clone="D08G04"
                     /tissue_type="Roots"
                     /dev_stage="Seedlings"
                     /clone_lib="cDNA Peking library 2, 4 day SCN3"
                     /note="Vector: pBluescript SK-; cDNA clones from mRNA
                     extracted from Peking roots 2 and 4 days past invasion."
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 9;
  Best Local Similarity   25.0%;  Pred. No. 4.2e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 14
CA851674/c
LOCUS       CA851674                  9 bp    mRNA    linear   EST 01-AUG-2003
DEFINITION  D16C10_F22_05.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
            cDNA clone D16C10 5', mRNA sequence.
ACCESSION   CA851674
VERSION     CA851674.1  GI:33388467
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Alkharouf,N.W., Khan,R. and Matthews,B.F.
  TITLE     Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharon@ba.ars.usda.gov.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Peking"
                     /db_xref="taxon:3847"
                     /clone="D16C10"
                     /tissue_type="Roots"
                     /dev_stage="Seedlings"
                     /clone_lib="cDNA Peking library 2, 4 day SCN3"
                     /note="Vector: pBluescript SK-; cDNA clones from mRNA
                     extracted from Peking roots 2 and 4 days past invasion."
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 6;  Length 9;
  Best Local Similarity   25.0%;  Pred. No. 4.2e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 15
CNS06E5N/c
LOCUS       CNS06E5N                  9 bp    DNA     linear   GSS 17-JUN-2001
```

```
DEFINITION  T3 end of clone AR0AA018H04 of library AR0AA from strain CBS 732 of
            Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION   AL394689
VERSION     AL394689.1  GI:12145788
KEYWORDS    GSS.
SOURCE      Zygosaccharomyces rouxii
  ORGANISM  Zygosaccharomyces rouxii
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 9)
  AUTHORS   de Montigny,J., Straub,M., Potier,S., Tekaia,F., Dujon,B.,
            Wincker,P., Artiguenave,F. and Souciet,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 8.
            Zygosaccharomyces rouxii
  JOURNAL   FEBS Lett. 487 (1), 52-55 (2000)
  MEDLINE   20584718
   PUBMED   11152883
REFERENCE   3  (bases 1 to 9)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Zygosaccharomyces rouxii"
                     /mol_type="genomic DNA"
                     /strain="CBS 732"
                     /db_xref="taxon:4956"
                     /clone="AR0AA018H04"
                     /clone_lib="AR0AA"
                     /note="end : T3"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 9;
  Best Local Similarity   25.0%;  Pred. No. 4.2e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 16
CL314040
LOCUS       CL314040                   9 bp    DNA     linear   GSS 01-MAR-2004
DEFINITION  mth2-130015_T7 Medicago truncatula BAC end sequences Medicago
            truncatula genomic 5', genomic survey sequence.
ACCESSION   CL314040
VERSION     CL314040.1  GI:44831714
KEYWORDS    GSS.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Jakab,J., Deak,G., Kevei,Z., Karchesz,K., Sarai,E., Kiss,P.,
            Kereszt,A., Kalo,P., Endre,G. and Kiss,G.B.
  TITLE     Medicago Truncatula BAC end sequencing
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Deak,G.
            Alfalfa Genomics Group; Medicago Genetics Group
            Agricultural Biotechnology Center; Biological Research Center
            P.O. Box 411, Hungary, H-2100 Godollo, Szent-Gyorgyi Albert ut 4.;
            P.O. BOX 521, Hungary, H-6701 Szeged, Temesvari krt. 62
            Tel: 3628526142
            Fax: 3628526193
            Email: gdeak@abc.hu
            Plate: 130  row: O  column: 15
            Seq primer: T7 Forward
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Medicago truncatula"
                     /mol_type="genomic DNA"
                     /cultivar="Jemalong"
                     /isolate="A17"
                     /db_xref="taxon:3880"
                     /sex="Hermaphrodite"
                     /clone_lib="Medicago truncatula BAC end sequences"
                     /note="Organ: Leaf; Vector: pBelo11; Site_1: HindIII;
                     Site_2: HindIII; Construction of a bacterial artificial
                     chromosome library of Medicago truncatula and
                     identification of clones containing ethylene-response
                     genes. Theor Appl Genet (1999) 98: 638-646 Y.-W.,Nam;
                     R.V.,Penmetsa; G.,Endre; P.,Uribe; D.,Kim; D.R.,Cook"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 9;
  Best Local Similarity   25.0%;  Pred. No. 4.2e+09;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 9


RESULT 17
AJ587649
LOCUS       AJ587649                  10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            304P05, genomic survey sequence.
ACCESSION   AJ587649
VERSION     AJ587649.1  GI:37937273
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
```

```
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="304F05"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 7


RESULT 18
AJ587650
LOCUS       AJ587650                 10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            304F06, genomic survey sequence.
ACCESSION   AJ587650
VERSION     AJ587650.1  GI:37937274
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="304F06"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTCG 7


RESULT 19
AJ593578/c
LOCUS       AJ593578                 10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            383D03, genomic survey sequence.
ACCESSION   AJ593578
VERSION     AJ593578.1  GI:37943202
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="383D03"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN
```

```
  Query Match            90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity  25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 20
AJ594077/c
LOCUS       AJ594077                  10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            392E10, genomic survey sequence.
ACCESSION   AJ594077
VERSION     AJ594077.1  GI:37943701
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="392E10"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity  25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTCG 3


RESULT 21
AJ594650/c
LOCUS       AJ594650                  10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            403C10, genomic survey sequence.
ACCESSION   AJ594650
VERSION     AJ594650.1  GI:37944274
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="403C10"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity  25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTCG 2


RESULT 22
AJ599592/c
LOCUS       AJ599592                  10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            490B05, genomic survey sequence.
ACCESSION   AJ599592
VERSION     AJ599592.1  GI:37949220
KEYWORDS    GSS; right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
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  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="490B05"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     right border"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 2


RESULT 23
AJ599908
LOCUS       AJ599908                 10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            496D12, genomic survey sequence.
ACCESSION   AJ599908
VERSION     AJ599908.1  GI:37949536
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="496D12"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          1 TTCG 4


RESULT 24
AJ600523/c
LOCUS       AJ600523                 10 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            508B03, genomic survey sequence.
ACCESSION   AJ600523
VERSION     AJ600523.1  GI:37950151
KEYWORDS    GSS; right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 10)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
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                     /db_xref="taxon:3702"
                     /clone="508B03"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .10
                     /note="T-DNA flanking sequence
                     right border"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 25
CL435887
LOCUS       CL435887                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST1710-2.seq MICB1 Mus musculus genomic clone PST1710-2.seq,
            genomic survey sequence.
ACCESSION   CL435887
VERSION     CL435887.1  GI:45570025
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST1710-2.seq
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST1710-2.seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTCG 5


RESULT 26
CL436026
LOCUS       CL436026                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2176-NR.Seq MICB1 Mus musculus genomic clone PST2176-NR.Seq
            similar to Rpl27a, genomic survey sequence.
ACCESSION   CL436026
VERSION     CL436026.1  GI:45570294
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2176-NR.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST2176-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 27
CL436141/c
LOCUS       CL436141                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2390-NL.Seq MICB1 Mus musculus genomic clone PST2390-NL.Seq
            similar to Rps25, genomic survey sequence.
ACCESSION   CL436141
VERSION     CL436141.1  GI:45570576
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
```

```
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2390-NL.Se
            q
            Class: Gene Trap.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="129 sv"
                      /db_xref="taxon:10090"
                      /clone="PST2390-NL.Seq"
                      /sex="Male"
                      /cell_type="Embryonic stem cell"
                      /cell_line="D3H (J1 subclone)"
                      /clone_lib="MICB1"
                      /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          8 TTTG 5


RESULT 28
CL436159
LOCUS       CL436159                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2429-NR.Seq MICB1 Mus musculus genomic clone PST2429-NR.Seq,
            genomic survey sequence.
ACCESSION   CL436159
VERSION     CL436159.1  GI:45570649
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2429-NR.Se
            q
            Class: Gene Trap.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="129 sv"
                      /db_xref="taxon:10090"
                      /clone="PST2429-NR.Seq"
                      /sex="Male"
                      /cell_type="Embryonic stem cell"
                      /cell_line="D3H (J1 subclone)"
                      /clone_lib="MICB1"
                      /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          2 TTTG 5


RESULT 29
CL436183/c
LOCUS       CL436183                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2465-NL.Seq MICB1 Mus musculus genomic clone PST2465-NL.Seq
            similar to Rps25, genomic survey sequence.
ACCESSION   CL436183
VERSION     CL436183.1  GI:45570727
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2465-NL.Se
            q
            Class: Gene Trap.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="129 sv"
                      /db_xref="taxon:10090"
                      /clone="PST2465-NL.Seq"
                      /sex="Male"
                      /cell_type="Embryonic stem cell"
                      /cell_line="D3H (J1 subclone)"
                      /clone_lib="MICB1"
                      /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          8 TTTG 5


RESULT 30
CL436207
LOCUS       CL436207                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2511-NR.Seq MICB1 Mus musculus genomic clone PST2511-NR.Seq
            similar to Snrp70, genomic survey sequence.
ACCESSION   CL436207
VERSION     CL436207.1  GI:45570779
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2511-NR.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST2511-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity  25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 31
CL436277
LOCUS       CL436277                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2644-NR.Seq MICB1 Mus musculus genomic clone PST2644-NR.Seq
            similar to Rpl27a, genomic survey sequence.
ACCESSION   CL436277
VERSION     CL436277.1  GI:45570921
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2644-NR.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST2644-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity  25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          3 TTTG 6


RESULT 32
CL436725
LOCUS       CL436725                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST3688-NR.Seq MICB1 Mus musculus genomic clone PST3688-NR.Seq
            similar to Hnrpu, genomic survey sequence.
ACCESSION   CL436725
VERSION     CL436725.1  GI:45571809
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST3688-NR.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST3688-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match            90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity  25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 9
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RESULT 33
CL437147/c
LOCUS       CL437147                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST4582-NL.Seq MICB1 Mus musculus genomic clone PST4582-NL.Seq
            similar to Rfxank, genomic survey sequence.
ACCESSION   CL437147
VERSION     CL437147.1  GI:45572623
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST4582-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST4582-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db         10 TTTG 7


RESULT 34
CL437213
LOCUS       CL437213                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST4731-NL.Seq MICB1 Mus musculus genomic clone PST4731-NL.Seq,
            genomic survey sequence.
ACCESSION   CL437213
VERSION     CL437213.1  GI:45572747
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST4731-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST4731-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          7 TTTG 10


RESULT 35
CL437237/c
LOCUS       CL437237                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST4801-NL.Seq MICB1 Mus musculus genomic clone PST4801-NL.Seq
            similar to Nup153, genomic survey sequence.
ACCESSION   CL437237
VERSION     CL437237.1  GI:45572787
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST4801-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST4801-NL.Seq"
                     /sex="Male"
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/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"
ORIGIN

Query Match 90.0%; Score 3.6; DB 9; Length 10;
Best Local Similarity 25.0%; Pred. No. 4.3e+07;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 7 TTTG 4

RESULT 36
CL437245/c
LOCUS CL437245 10 bp DNA linear GSS 18-MAR-2004
DEFINITION PST4835-NL.Seq MICB1 Mus musculus genomic clone PST4835-NL.Seq similar to Nup153, genomic survey sequence.
ACCESSION CL437245
VERSION CL437245.1 GI:45572801
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hicks,G.G.
TITLE www.EScells.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from http://140.193.242.7/esdb/public_search_frame.php?PST=PST4835-NL.Seq
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST4835-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"
ORIGIN

Query Match 90.0%; Score 3.6; DB 9; Length 10;
Best Local Similarity 25.0%; Pred. No. 4.3e+07;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 7 TTTG 4

RESULT 37
CL437288
LOCUS CL437288 10 bp DNA linear GSS 18-MAR-2004
DEFINITION PST4926-NR.Seq MICB1 Mus musculus genomic clone PST4926-NR.Seq, genomic survey sequence.
ACCESSION CL437288
VERSION CL437288.1 GI:45572879
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hicks,G.G.
TITLE www.EScells.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from http://140.193.242.7/esdb/public_search_frame.php?PST=PST4926-NR.Seq
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST4926-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"
ORIGIN

Query Match 90.0%; Score 3.6; DB 9; Length 10;
Best Local Similarity 25.0%; Pred. No. 4.3e+07;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UUYG 4
:::|
Db 3 TTTG 6

RESULT 38
CL437389/c
LOCUS CL437389 10 bp DNA linear GSS 18-MAR-2004
DEFINITION PST5280-NL.Seq MICB1 Mus musculus genomic clone PST5280-NL.Seq similar to Zfp162, genomic survey sequence.
ACCESSION CL437389
VERSION CL437389.1 GI:45573053
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hicks,G.G.
TITLE www.EScells.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES

```
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST5280-NL.Se
            q
            Class: Gene Trap.
FEATURES                Location/Qualifiers
     source             1. .10
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="129 sv"
                        /db_xref="taxon:10090"
                        /clone="PST5280-NL.Seq"
                        /sex="Male"
                        /cell_type="Embryonic stem cell"
                        /cell_line="D3H (J1 subclone)"
                        /clone_lib="MICB1"
                        /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          9 TTTG 6


RESULT 39
CL437824
LOCUS       CL437824                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6362-NR.Seq MICB1 Mus musculus genomic clone PST6362-NR.Seq,
            genomic survey sequence.
ACCESSION   CL437824
VERSION     CL437824.1  GI:45573802
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6362-NR.Se
            q
            Class: Gene Trap.
FEATURES                Location/Qualifiers
     source             1. .10
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="129 sv"
                        /db_xref="taxon:10090"
                        /clone="PST6362-NR.Seq"
                        /sex="Male"
                        /cell_type="Embryonic stem cell"
                        /cell_line="D3H (J1 subclone)"
                        /clone_lib="MICB1"
                        /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 8


RESULT 40
CL437844/c
LOCUS       CL437844                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6396-NR.Seq MICB1 Mus musculus genomic clone PST6396-NR.Seq,
            genomic survey sequence.
ACCESSION   CL437844
VERSION     CL437844.1  GI:45573837
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6396-NR.Se
            q
            Class: Gene Trap.
FEATURES                Location/Qualifiers
     source             1. .10
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="129 sv"
                        /db_xref="taxon:10090"
                        /clone="PST6396-NR.Seq"
                        /sex="Male"
                        /cell_type="Embryonic stem cell"
                        /cell_line="D3H (J1 subclone)"
                        /clone_lib="MICB1"
                        /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          4 TTTG 1


RESULT 41
CL437917/c
LOCUS       CL437917                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6521-NL.Seq MICB1 Mus musculus genomic clone PST6521-NL.Seq,
            genomic survey sequence.
ACCESSION   CL437917
VERSION     CL437917.1  GI:45573963
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6521-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST6521-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          7 TTTG 4


RESULT 42
CL437998/c
LOCUS       CL437998                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6636-NL.Seq MICB1 Mus musculus genomic clone PST6636-NL.Seq
            similar to Rps25, genomic survey sequence.
ACCESSION   CL437998
VERSION     CL437998.1  GI:45574123
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6636-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST6636-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          8 TTTG 5


RESULT 43
CL437999/c
LOCUS       CL437999                  10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6637-NL.Seq MICB1 Mus musculus genomic clone PST6637-NL.Seq
            similar to Rps25, genomic survey sequence.
ACCESSION   CL437999
VERSION     CL437999.1  GI:45574124
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6637-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST6637-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          8 TTTG 5
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RESULT 44
CL438166
LOCUS       CL438166                 10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6939-NR.Seq MICB1 Mus musculus genomic clone PST6939-NR.Seq,
            genomic survey sequence.
ACCESSION   CL438166
VERSION     CL438166.1  GI:45574452
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6939-NR.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST6939-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          6 TTTG 9


RESULT 45
CL438191
LOCUS       CL438191                 10 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST6982-NL.Seq MICB1 Mus musculus genomic clone PST6982-NL.Seq
            similar to Gtf2a1, genomic survey sequence.
ACCESSION   CL438191
VERSION     CL438191.1  GI:45574499
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST6982-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST6982-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             90.0%;  Score 3.6;  DB 9;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 4.3e+07;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 UUYG 4
              :::|
Db          5 TTTG 8


Search completed: April  4, 2005, 12:51:20
Job time : 2048 secs
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